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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ONWATFOOKHIINT-PIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGV-INLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Liver;
Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (4002-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF242556; AAG31442.2; -.
HSSP; P22069; IONC.
                                                     01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase3 ribonuclease precursor.
Rana catesbeiana (Bull frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase6 ribonuclease precursor.
Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C., "Purification and cloning of cytotoxic ribonucleases from Rana catesbeinana (bullfrog).";
Nucleic Acids Res. 28+4097-4104(2000).
EMBL; AF242554; AAG31440.2; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.,
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                     9;
                                                                                                                                                                                                                                                                                                                                                                           37.2%; Score 223.5; DB 13; Length 128; 40.2%; Pred. No. 7e-18; Live 19; Mismatches 39; Indels 9;
                                                                                                                                                                                                                                                 GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                           24 128 RC-RNASE3 RIBONUCLEASE.
128 AA; 14517 MW; 2B14986082E0587D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 16, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                        128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 AA
                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                  Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 28:4097-4104(2000)
                                              Created)
                       PRT;
                                          01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                  45; Conservative
                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catesbeiana (bullfrog)
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                        NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=8400;
                                                                                                                                                         TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                 Q9DFY7:
                                                                                                                                                                                                                                                                                                                                SIGNAL
                     Q9DFY7
                                                                                                                                                                                                                                                                                                                      Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9DFY5
                                                                                                                                                                                                                                                                                                                                            CHAIN
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Q9DFY5
RESULT 11
             Q9DFY7
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                                                                                                                                                                                                                                                                                                                                                                1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                      79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
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                                                                                                                                                                                                                                                                                                                                                                                               24 QDWDTFQKKHLIDTKKVKCDVEMKKALF----DCKKTNTFIFARPPRVQALCKNIKDNTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ONWATFOOKHII--NTPIICN-TILDNNIYIVGGQCKRVNTFI-ISSATTVKAICTGVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 ONINAFMEKHIVKEGAETNCNOTIKDRNIRF-KNNCKFRNTFIHDTNGKKVKEMCAGIVK
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96069863; PubMed=7585965;
Kinoshita N., Minshull J., Kirschner M.W.;
"The identification of two novel ligands of the FGF receptor by a
Yeast screening method and their activity in Xenopus development.";
Cell 83:621-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 VLSRDVFYLPQCNRKKL---PCHYRLDGSTNTICLTCMKELPIHFAGVGKCP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 LN-VLSTTRFQLNTCTRTSITPRP--CPYSSRTETNYICVKCENQYPVHFAG 105
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8
                                                                                                                                                                                                                                                                       DB 13; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.8%; Score 161; DB 13; Length 169; 39.3%; Pred. No. 1.5e-10; ive 10; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                     Indels
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinoshita N., Kirschner M.W.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFIS9166; AAD41901.1; -.
HSSP; P00656; 1LSQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                         24 128 RC-RNASE6 RIBONUCLEASE.
128 AA; 14804 MW; AFEBFD67D266C7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                  ch 35.8%; Score 214.5; DB 13; l Similarity 38.4%; Pred. No. 7.7e-17; 43; Conservative 20; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą
                                                                                                                                                                       POTENTIAL
                                                                 Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 39.3 tes 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus.
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRL2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae;
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                           Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09W738;
                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9W738
                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 CKNGQPNCHQSNST-MNITDCRQTGGSKYPNCAYKTSQKQKYIIVACEGTPSVPVHFDGS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 AKFRRQHLDAGNSINSN-YCNLAMKRR-KMTHGRCKPVNTFIHESLEDVKAICSEKNIT
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 POTENTIAL.
170 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
18832 MW, ABGCE7E1E5549AA0 CRC64;
                                                                                                                                                                                                     Tragulus javanicus (Lesser Malay chevrotain).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Tragulina,
Tragulidae, Tragulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46; Indels 20;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=21347458; PubMed=11453981;

Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,

Warmels H.W., Beintem J.J.;

Warmels H.W., Beintem J.J.;

Wecretory ribonucleases in the primitive ruminant chevrotain

(Tragulus javanicus).";

Bur. J. Biochem. 268:3890-3897(2001).

Let. MILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

HSSP; PO0656; 1129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.3%; Score 128; DB 6; Length 170; 32.3%; Pred. No. 9.5e-07; cive 18; Mismatches 46; Indels 2
                                                                                                                                                      Brain-type ribonuclease ribonuclease precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0004519; F:endonuclease activity; IEA.
GO; GO:00145787; F:hydrclase activity; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA
INCERP: IRFO01427; RNaseA.
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Last sequence update)
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Last annotation update)
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                      170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00092; RNAse Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Endonuclease; Hydrolase; Nuclease; Signal.
                                                                              Created)
                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=NMRI;
MEDLINE=22493143; PubMed=12548285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                     01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00.000 (Tremblrel. 24, 01.JUN-2003 (Tremblrel. 24, 01.JUN-2003 (Tremblrel. 24, 01.OCT-2003 (Tremblrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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20
170 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 GRCP 110
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                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                               Q9BEC1;
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                      Q9BEC1
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Q80Z85
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Q9BEC1
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Search completed: May 7, 2004, 21:46:04 Job time: 31.2816 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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using sw model protein search, OM protein

7, 2004, 21:29:40 ; Search time 33.3695 Seconds May Run on:

(without alignments)
865.070 Million cell updates/sec

US-09-961-400-2 578 Title: Perfect score:

1 QDWLTFQKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1140673 seqs, 277566755 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

Published Applications AA:\*

| cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/2/pubpaa/US07\_BW PUB.pep:\*
| cgn2\_6/ptodata/2/pubpaa/US06\_BW PUB.pep:\*
| cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/2/pubpaa/US06\_BW PUB.pep:\*
| cgn2\_6/ptodata/2/pubpaa/US07\_BW PUB.pep:\*
| cgn2\_6/ptodata/2/pubpaa/US08\_BW PUB.pep:\*
| cgn2\_6/ptodata/2/pubpaa/US08\_BW PUBCOMB.pep:\*
| cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

/cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 2, Appli Sequence 6, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 11, Appli Sequence 11, Appli Sequence 13, Appli Sequence 13, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 8, Appli	
SUMMARIES ID	US-09-561-400-2 US-09-561-400-2 US-09-948-391A-6 US-09-948-391A-18 US-09-961-400-2 US-09-961-400-3 US-09-961-400-11 US-09-948-391A-11 US-09-948-391A-2 US-09-948-391A-2 US-09-961-400-13 US-09-948-391A-2 US-09-961-400-8 US-09-961-400-8 US-09-961-400-8 US-09-961-400-8 US-09-961-400-8	
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% Query Match Length DB	4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
% Query Match	10001 10001 10000	
Score	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	
Result No.	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	

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Indels

9 9

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62,1	3.01	equence requence 1 equence 1 equence 1	Sequence 21, Appl Sequence 22, Appl Sequence 22, Appl Sequence 24, Appl	26, 26, 17, 19, 2, 7	13. 5. 10. 25. 1
0 US-09-948-391A-9 US-10-153-882-2 US-09-986-119-1 US-09-918-887-1	US-10-461-713 US-09-986-119- US-09-918-887 US-09-948-391	US-09-961-400-17 US-09-961-400-17 US-09-961-400-17 US-09-961-400-19 US-09-948-391A-2	US- US- US- US-	US-09-948-391A-26 US-09-961-400-26 US-09-948-391A-17 US-09-948-391A-19 US-10-016-447-2 US-10-016-248-89	0. US-10-074-978-139 US-10-016-447-5 US-10-037-417-103 US-02-86-240-6 US-09-863-777-2 US-09-731-872-254
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### ALIGNMENTS

Sequence 2, Application US/09961400

Sequence 2, Application US/09961400

Publication No. US20030124131A1

SEGNERAL INRORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

CURRENT PILING DATE: 2001-09-25

CURRENT PILING DATE: 2001-09-25

FRIOR PAPLICATION NUMBER: 09/622,613

FRIOR APPLICATION NUMBER: 60/079-751

PRIOR APPLICATION NUMBER: 60/079-751

PRIOR APPLICATION NUMBER: 60/079-751

PRIOR APPLICATION NUMBER: 60/079-751

SEQ ID NO 2

SEQ ID NO 2

LENGTH: 104 Length 104; 100.0%; Score 578; DB 10; 100.0%; Pred. No. 1.2e-58; ive 0; Mismatches 0; Best Local Similarity 100. Matches 104; Conservative TYPE: PRT ORGANISM: Rana pipiens RESULT 1 US-09-961-400-2 US-09-961-400-2 Query Match

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US-09-961-400-28
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APPLICANT: RYBAK, GUSANNA M.
APPLICANT: GOLDBNBERG, DAVID M.
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: LOFICATION WORDER: US/09/961,400
CURRENT APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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US-U9-948-391A-6

Sequence 6, Application US/09948391A

Publication No. US20030027311A1

GENERAL INFORMATION:

APPLICANT: Newton, Dianne L.

APPLICANT: Newton, Dianne L.

APPLICANT: The United States of America

APPLICANT: The United States of America

APPLICANT: Department of Health and Human Services

ITLE OF INVENTION: Recombinant Anti-Tumor RNase

FILE REFERENCE: 015280-343110US

CURRENT APPLICATION NUMBER: US 60/079,751

PRIOR APPLICATION NUMBER: US 09/622,613

PRIOR APPLICATION NUMBER: US 09/622,613

SOFTWARE: PATENTIN OF ATE: 1999-03-26

PRIOR APPLICATION NUMBER: US 09/622,613

SOFTWARE: PATENTIN OF ATE: 1000-08-17

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 6

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; ORGANISM: Rana pipiens
US-09-961-400-6
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US-09-961-400-6
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Publication No. US20030124131A1

GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANA M.
APPLICANT: RYBAK, SUSANA M.
TITLE OF INVENTION: IMMUNCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICANTION NUMBER: US/09/961,400
CURRENT PILING DATE: 2001-09-25
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 2000-08-17
                                                                                                              QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Rana pipiens ribonuclease (RaPLR1) Clone 5alb cDNA; OTHER INFORMATION: insert
US-09-948-391A-28
                                                          Gaps
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Length 105;
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                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rewich, Dianne D.
APPLICANT: Rewich, Dianne D.
APPLICANT: Newton, Dianne D.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
ITILE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: W 60/079,751
PRIOR APPLICATION NUMBER: W 60/079,751
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER: OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 578; DB 10; 100.0%; Pred. No. 1.6e-58;
100.0%; Score 578; DB 10; 100.0%; Pred. No. 1.3e-58;
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                                                          0; Mismatches
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. Sequence 28, Application US/09948391A
. Publication No. US20030027311A1
. GENERAL INFORMATION:
  Query Match
Best Local Similarity 100.0
Matches 104; Conservative
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Matches 104; Conservative
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TYPE: PRT
ORGANISM: Rana pipiens
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Best Local S:
Matches 103,
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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNCCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS.
FILE REPERENCE: 018733/1059
CURRENT APPLICATION NUMBER: 09/622,613
FRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 9
TENTINE OF SEC ID NOS: 43
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~heg 0; Indels
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99.0%; Pred. No. 3e-58;
cive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                         0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
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US-09-948-391A-11
Sequence 11, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09961400 Publication No. US20030124131A1 GENERAL INFORMATION:
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                                                                                                                                                             TYPE: PRT
ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Rana pipiens
US-09-961-400-9
                                                                                                                                                                                                                                                                  Best Local Similarity
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Matches 103;
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US-09-961-400-9
                                                                                                                                                                                                                                               Query Match
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Sequence 11, Application US/09961400
| Publication No. US20030124131A1
| SEMENAL INFORMATION: US20030124131A1
| APPLICANT: RYBAK, SUSANNA M.
| APPLICANT: GOLDENBERG, DAVID M.
| APPLICANT: GOLDENBERG, DAVID M.
| APPLICANT: NEWTON, DIANNE L.
| TITLE OF INVENTION: CELLS
| TITLE OF INVENTION: CELLS
| TITLE OF INVENTION: USLOS
| TITLE REFERENCE: 018733/1059
| CURRENT APPLICATION NUMBER: 0201-09-25
| CURRENT FILING DATE: 2000-08-17
| PRIOR FILING DATE: 1999-03-26
| NUMBER OF SEQ ID NOS: 43
| SOFTWARE: PATCHIT OF VERY SEQ ID NOS: 43
| SEQ ID NOS: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Description of Artificial Sequence:Rana pipiens; OTHER INFORMATION: ribonuclease with Gln1Ser substitution CTHER INFORMATION: (recombinant RapLR1 Q1S)
US-09-948-391A-11
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Pred. No. 4.7e-58;
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APPLICANT: as represented by The Secretary of the APPLICANT: Department of Health and Human Services TITLE OF INVENTION: Recombinant Anti-Tumor RNase; FILE REFERENCE: 015280-343110US; CURRENT FILING DATE: 2002-05-10; PRIOR APPLICATION NUMBER: US 60/079,751 PRIOR PILING DATE: 1998-03-27; PRIOR APPLICATION NUMBER: W0 PCT/US99/06641; PRIOR FILING DATE: 1999-03-26; PRIOR PELICATION NUMBER: W0 OFCT/US99/06641; PRIOR PILING DATE: 1999-03-26; PRIOR PELICATION NUMBER: W1 09/622,613; PRIOR FILING DATE: 2000-08-17; NUMBER: OF SEQ ID NOS: 43; SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0%; Pred. No. 4.7e-58; Matches 103; Conservative 0; Mismatches 0;
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Conservative 0;
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Newton, Dianne L. The United States of America

APPLICANT: Rybak, Susanna M. APPLICANT: Newton, Dianne L. APPLICANT: The United State

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; Sequence 2, Application US/09948391A
; Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US 60/079,751
FRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
SPRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFFWARE: Patentin Ver. 2.0
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APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
                                                                                                  99.1%; Score 573; DB 10;
100.0%; Pred. No. 4.7e-58;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
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Best Local Similarity 99.0
Matches 103; Conservative
                                                                                                                                              Best Local Similarity 100.
Matches 103; Conservative
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ORGANISM: Rana pipiens
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US-09-948-391A-4
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US-09-961-400-13
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                                                                                                              Query Match
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APPLICANT: RYBAK, SUGANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: OFFICE 10873/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: OFfice 10873/1059
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: FCT/US99/06641
PRIOR APPLICATION NUMBER: EC/079,751
PRIOR APPLICATION NUMBER: EC/079,751
PRIOR APPLICATION NUMBER: EC/079,751
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR APPLICATION NUMBER: 2000-08-17
SPRIOR PRILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE PATENTING DATE: 1908-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 99.1%; Score 573; DB 10; Length 105; Best Local Similarity 100.0%; Pred. No. 4.7e-58; Matches 103; Conservative 0; Mismatches 0; Indels (
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62 BFYLSDCNVTSRPCKYKIKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                FULLIAGACION NO. USZUUJUUZ/JIIA]

GENERAL INFORMATION:

APPLICANT: Nybak, Susanna M.

APPLICANT: Newton, Dianne L.

APPLICANT: The United States of America

APPLICANT: The United States of America

APPLICANT: The United States of America

APPLICANT: Department of Health and Human Services

TITLE OF INVENTION: Recombinant Anti-Tumor RNase

FILE REFERENCE: 015280-343110US

CURRENT FPLING DATE: 2002-05-10

PRIOR APPLICATION NUMBER: US 60/079,751

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 2000-08-17

WUMBER: OF SEQ ID NOS: 43

SOUTHWANDER: US 80/020-05

NUMBER: OF SEQ ID NOS: 43

SOUTHWANDER: US 80/020-06-17
                                                                                                                                                                                                 US-09-948-391A-13; Sequence 13, Application US/09948391A; Publication No. US20030027311A1
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; Sequence 13. Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0
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LENGIH: 105
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TYPE: PRT

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US-09-961-400-8
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Sequence 8, Application US/09961400
Fublication No. US20030124131A1
FUBLICANT: NEWTON, USZONANA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: MENTON, DIANNE L.
ITILE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
ITILE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
FRIOR PELLING DATE: 2000-08-11
FRIOR PELLING DATE: 1999-03-26
FRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTION NUMBER: 60/079,751
FRIOR FILING DATE: 1998-03-26
SOFTWARE: PATENTION NUMBER: 201-26
SOFTWARE: PATENTION NUMBER: 60/079,751
FRIOR FILING DATE: 1998-03-26
SOFTWARE: PATENTION NUMBER: 60/079,751
FRIOR FILING DATE: 1998-03-26
SOFTWARE: PATENTIN NUMBER: 60/079,751
FRIOR FILING DATE: 1998-03-26
SOFTWARE: PATENTING NUMBER: 60/079,751
FRIOR FILING DATE: 1998-03-26
SOFTWARE: PATENTING NUMBER: 60/079,751
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Pred. No. 3.9e-57;
1; Mismatches 2;
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97.1%;
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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 97.1'
Matches 101; Conservative
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APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

FILE REPERBUCE: 018733/1059

CURRENT APPLICATION NUMBER: 05/62,613

PRIOR APPLICATION NUMBER: 09/62,613

PRIOR APPLICATION NUMBER: 09/62,613

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR PILING DATE: 1999-03-26

PRIOR PILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens; OTHER INFORMATION: ribonuclease with Met23Leu substitution; CTHER INFORMATION: (recombinant RaPLRI Met23Leu)
US-09-948-391A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.4%; Score 569; DB 10; Length 104; 98.1%; Pred. No. 1.3e-57; ive 1; Mismatches 1; Indels
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Pred. No. 1.3e-57;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: W0 PCT/US99/06641
PRIOR APPLICATION NUMBER: W0 99/622,613
PRIOR PILING DATE: 2000-08-17
PRIOR PLING DATE: 2000-08-17
WUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09961400 Publication No. US20030124131A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.4%;
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Best Local Similarity 98.1:
Matches 102; Conservative
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Matches 102; Conservative
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US-09-961-400-4
                                                                                                                                                                                                                                     SEQ ID NO 4
LENGIH: 104
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Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens OTHER INFORMATION: ribonuclease with Met at position 1 and Met24Leu OTHER INFORMATION: substitution (recombinant Met(-1) RapErl Met23Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                        Sequence 8, Application US/09948391A

| Publication No. US20030027311A1
| GENERAL INFORMATION:
| APPLICANT: Newton, Dianne L.
| APPLICANT: The United States of America APPLICANT: Department of Health and Human Services ITILE OF INVENTION: Recombinant Anti-Tumor RNase FILE REFERENCE: 015280-343110US
| CURRENT APPLICATION NUMBER: US/09/948,391A |
| PRIOR FILING DATE: 1998-03-27 |
| PRIOR FILING DATE: 1998-03-27 |
| PRIOR FILING DATE: 1999-03-26 |
| PRIOR FILING DATE: 1999-03-26 |
| PRIOR FILING DATE: 2000-08-17 |
| NUMBER OF SEQ ID NOS: 43 |
| SOFFWARE: Patentin Ver. 2.0 |
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Matches 101; Conservative
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61 SBFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104 δ ΩD

Search completed: May 7, 2004, 21:51:55 Job time : 33.3695 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- protein search, using sw model OM protein 7, 2004, 21:25:55 ; Search time 44.363 Seconds (without alignments) 662.376 Million cell updates/sec Run on:

US-09-961-400-2

578 1 ODWLTFOKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104 Perfect score: Seguence:

**BLOSUM62** Scoring table:

1586107 seqs, 282547505 residues Gapop 10.0 , Gapext 0.5 Searched:

of hits satisfying chosen parameters:

Total number

1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* A Geneseq 29Jan04:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2004s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

	Description	Aav28865 Rana Dini	7 Recor			-			Aaw06544 Antitumou	Aaw30301 Recombina	Aab31666 Amino aci		LO.	Aar12344 Protein w	_		_	Aaw06543 Antitumou	Aaw88233 Rana pipi	Aay33322 Frog onco	Aaw35123 R. pipien	Aav39400 Recombina	2	2	2 R	Aaw35117 R. pipien
SUMMARIES	ID	AAY28865	AAY28867	AAY28879	AAY28866	AAY28869	AAY28870	AAY28871	AAW06544	AAW30301	AAB31666	ABG32650	AAW35126	AAR12344	AAR47303	AAW00736	AAW14065	AAW06543	AAW88233	AAY33322	AAW35123	AAY39400	AAW35125	AAW35130	AAW35122	AAW35117
	DB	2	N	7	N	7	7	7	7	N	4	2	7	7	N	7	7	7	7	7	N	7	7	7	7	7
	Length	104	105	127	104	105	104	105	104	104	104	104	379	104	104	104	104	104	104	104	105	105	355	358	106	107
oks	Query Match	100.0	100.0	100.0	99.5	99.2	φ.	99.1	96.5	96.2	96.2	96.2	96.2	95.7	95.7	95.7	95.7	95.7	95.7	95.7	95.7	95.7	95.7	95.7	95.3	95.3
	Score	578	578	578	575	575	573	573	558	256	556	556	556	553	553	553	553	553	553	553	553	553	553	553	551	551
	Result No.	П	73	3	4	ហ	9	7	œ	o,	10	11	12	13	14	15	16		18	19	20	21	22	23	24	25

5.50	Aaw35123 K. Piplen Aaw35129 R. piplen Aaw35132 R. piplen Aaw30302 Recombina	Aaw18224 Antitumou Aab31667 Amino aci Abq31617 Northern	Aaw35115 R. pipien Aaw35116 R. pipien Aaw35127 R. pipien		
AAW35118 AAW35134 AAW35135	AAW35129 AAW35132 AAW30302	AAW18224 AAB31667 ABG31617	AAW35115 AAW35116 AAW35127	AAW35131 AAW35120 AAW35128	AAW35121 AAW35119 AAW88234 AAY33321
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112 251 251 254	355 366 104	104 104 104	105 105 358	365 107 360	111 83 83 111
9999 8000 8000 8000 8000 8000 8000 8000	95.3 95.3 95.3	9. 4. 9. 8. 4. 9. 8. 8. 8.	94.5 93.5	93.8 91.2 84.8	83.7 77.0 77.0 50.0
551 551 551 551	551 551 550	548 548 548	546 546 542	542 527 490	483.5 445 445 289
26 27 28	330	60 60 60 60 44 73	36 37 88	39 41	44 44 45

### ALIGNMENTS

RESULT 1 AAY28865

AAY28865 standard; protein; 104 AA.

AAY28865; 

(first entry) 25-JAN-2000

Rana pipiens liver ribonuclease (RaPLR1).

Rana pipiens liver ribonuclease, RaPLR1; covalently bound; LL2 antibody; ligard binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog; human chorionic gonddotrophin; hCG; recombinant ribonuclease; RNase; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.

Rana pipiens

W09950398-A2

07-OCT-1999.

99WO-US006641. 26-MAR-1999;

98US-0079751P. 27-MAR-1998; (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Newton DL; Rybak SM,

WPI; 1999-610847/52.

N-PSDB; AAZ08124

for New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.

Claim 1; Page 55; 71pp; English

The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein. Carboxy terminal end of RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hG3) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases

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Best Local Similarity
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                                                                                                                                                            1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                           Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cel Kaposi s sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease.
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
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0
                                                100.0%; Score 578; DB 2; Length 104; 100.0%; Pred. No. 4.6e-62;
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                                                                                                                                                                                                                                                                     SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                    SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                         Indels
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                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY28867 standard; protein; 105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 34; Page 57; 71pp; English.
                                                                            100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant Met (-1) RaPLR1
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                                                                                                   Matches 104; Conservative
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                                                                         Best Local Similarity
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Sequence 104 AA;
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Synthetic.
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                                                                                                                                                                                                                                                                     61
                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
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DB 2; Length 105;

100.0%; Score 578;

Sequence 105 AA;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                              LL2 antibody, ligand binding moiety; CD22; cancerous B cell; onconase;
Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer;
recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
                                                09
                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RaPLR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                Rana pipiens ribonuclease Clone 5alb; RaPLR1; covalently bound; RNase;
                                                                     QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                              QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
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                                                                                                                                      SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                SEFYLSDCNVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
                 Indels
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100.0%; Pred. No. 4.6e-62; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .23
/label= Signal_peptide
/note= "Putative"
                                                                                                                                                                                                                                                                                                                               Rana pipiens Clone 5alb ribonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 69; 71pp; English.
                                                                                                                                                                                                                                  AAY28879 standard; protein; 127 AA
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                 Conservative
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N-PSDB; AAZ08136.
                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease.
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                 104;
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ID AAY
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The present sequence is a recombinant Rana piplens ribonuclease (RaPIRI) protein with MerSileu. Carboxy terminal end of recombinant RaPIRI has a covalently bound ligand binding moiety, which can be a Li2 antibody directed against CD22 on cancerous B cells or human chorionic gonadorrophin (MoG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in hacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treament of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                  Recombinant Rana pipiens ribonuclease; RaPLR1 Met23Leu; covalently bound; Liz antibody; ligand binding molety; CD22, cancerous B cell; RNase; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                    24 ODWLTFOKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                        QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                           0;
            Length 127;
                                                                                                                                                      SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
                                                                                                                                    SEFYLSDCNVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild type Met replaced with Leu"
           Score 578; DB 2;
Pred. No. 5.9e-62;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                      Recombinant RaPLR1 Met23Leu amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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100.0%; Suc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.5%; Scor.
99.0%; Pred
1; 1
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                                                                                                                                                                                                                                           AAY28866 standard; protein; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US006641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0079751P
                                                                                                                                                                                                                                                                                                        (first entry)
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM, Newton DL;
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                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ08125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                        25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                             pipiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9950398-A2
                Ma.
Local 5.
104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                         AAY28866;
                                                                        Н
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              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rybak
                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rana
                                                                                                                                                                                                                              RESULT 4
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The present sequence is a recombinant Rana pipiens ribonuclease protein (RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancercus B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "(His)6 histidine tag attached to N-terminal Met"
                                                                                                                                                                                                                                                                                                                       Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1; CD2; covalently bound; LL2 antibody; ligand binding moiety; RNase; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease.
                1 ODWLTFQKKHLTNTRDVDCNNILSTWLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTF1YSRPEPVKA1CKG11ASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Met not found in wild type RaPLR1"
                                                                                   61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                 SEFYLSDCNVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                       Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 575; DB 2;
Pred. No. 1.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                     AAY28869 standard; protein; 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 59; 71pp; English
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99.0%;
                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Newton DL;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                          Rana pipiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9950398-A2
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                                                                                                                                                                                                                       AAY28869;
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                                                                                                                                                                       AAY28869
                                                                                                                                                     RESULT
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for

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Gaps

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Score 575; DB 2; Length 104; Pred. No. 1.1e-61; 1; Mismatches 0; Indels

Conservative

Local Similarity

Best Local Sim Matches 103;

Query Match

104 104 cell;

103;

Matches

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61

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AAY28870;

RESULT 6 AAY28870

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The present sequence is a recombinant Rana pipiens ribonuclease (RaPLRI) protein with Met at position I and Gln28er. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD2 on cancerous B cells or human chorionic gonadorrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an Neterminal methionine due to the presence of a signal peptide that is proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
  DWLIFQKKHITNIRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
                                                                                                                                                                                                                                                                                                                                                      Recombinant Met (-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cel Kaposi; s sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease; RNBSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 573; DB 2; Length 105; Pred. No. 1.9e-61; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Met not found in wild type RaPLR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                                                                                                                 Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.
                                                                                    EFYLSDCHVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                             EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                   AAY28871 standard; protein; 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.15,
100.0%; Pre
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                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rana pipiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                             62
                                                                                                    62
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Best Local S
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                                                                                                                                                                            AAY2887
                                                                                                                                                            RESULT
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                                         09
                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant Rana pipiens ribonuclease, RaPLRI GlnISer; covalently bound; LLZ antibody; Llagand binding molety, CD2; cancerous B cell; frog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; combinant ribonuclease; cytotoxic fusion protein; cancer; RNase;
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                                    QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                         2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 104;
                                                                                                                                         SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Pred. No. 1.9e-61;
                                                                                                                                                                                                                                                                                                                                                                       Recombinant RaPLR1 Gln1Ser amino acid sequence.
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100.0%; Pred. No. 1...
... 0; Mismatches
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                    AAY28870 standard; protein; 104
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Best Local Similarity 100.
Matches 103; Conservative
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rana pipiens.
Synthetic.
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07-OCT-1999

Rybak SM,

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for

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The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW18224, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW06543) that have been isolated from Rana pipiens occytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer treatment of tumours
 3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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Pred. No. 1.2e-59;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antitumour proteins from Rana pipiens oocyte(s) - have fer
disadvantages than chemotherapy, surgery and radiotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104
                                               EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                            62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                              Antitumour protein from Rana pipiens oocytes.
                                                                                                                                                                                                                                          Tumour; chemotherapy; radiotherapy; frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 104 AA
                                                                                                                           AAW06544 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Page 28; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                       96WO-US008304
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nes 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-043063/04
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                                                                                                                                                                                                                                                                                               WO9639428-A1
                                                                                                                                                                                                                                                                      Rana pipiens
                                                                                                                                                                                                                                                                                                                                                         03-JUN-1996;
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                                                                                                                                                       AAW06544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Ardelt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW30301
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                                                                                               RESULT 8
AAW06544
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This sequence represents a recombinant Onc protein comprising a 104 amino acid sequence having Gln at position 1. Onc, a ribonuclease from Rana pipiens cocytes, is known as an antitumour agent (e.g. for treating pancreatic cancer) and inhibitor of human immunodeficiency virus type-1 replication. It can be used therapeutically or as a cell-culture selection agent, e.g. to identify gene therapy compositions able to inhibit tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "this Gln is autocyclised to pyroglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant Onc protein with glutamine residue at position 1 - useful antitumour and antiviral agent, also as cell culture selection agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                           Onc; oncanase; ribonuclease; frog; antitumour; pancrea
human immunodeficiency virus type-1; HIV1; replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a frog ribonuclease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ardelt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 556; DB 2;
Pred. No. 2.1e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boix E,
                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Frog; ribonuclease; ranpirnase; RNase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 28; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vasandani VM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 100; Conservative
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/note= '
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                              04-APR-1997;
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                                                                                                                    Rana pipiens
                                                                                                                                                                         WO9738112-A1
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                                                                                                                                                                                                                                   16-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          foule RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB31666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB31666
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                                                                                                                                                                                                                                                                                      (RNase). The specification describes a synthetic ribonuclease protein, in which the addition of cysteine in the ribonuclease facilitates the which the addition of cysteine in the ribonuclease facilitates the chemical linking of a targeting molecule by the single reactive sulfinydryl group. The specification also describes a method for the production of rampirase using DNA technology instead of processing biological material. The re-engineering of the protein molecule allows easier attachment to a targeting molecule thereby making it possible for the ribonuclease to be delivered to a particular cell receptor where it might be most effective
                                                                                                                                                        New nucleic acids encoding a ribonuclease (Rnase), useful for the precise targeting of Rnase to a predetermined cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                          sequence represents a frog ribonuclease protein (ranpirnase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Constructing isolated nucleic acid encoding ribonuclease, by subjecting desired recombinant plasmid DNA to different site-directed mutations to produce nucleic acid, using different polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Northern leopard frog; ranpirnase; site-directed mutation; ribonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEFYLSDCNVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 556; DB 4; Le
Pred. No. 2.1e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Northern leopard frog ranpirnase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG32650 standard; protein; 104 AA.
                                                                                                                                                                                                                          Claim 1; Col 5-6; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.2%;
96.2%;
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                (ALFA-) ALFACELL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ALFA-) ALFACELL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-664633/71.
                                                                                                          WPI; 2001-167808/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6423515-B1
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                                                                                                                                                                                                                                                                     The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saxena SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protocols
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                                                              Saxena
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ð g à g Claim 1; Col 5-6; 8pp; English.

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             nucleic acid encoding ribonuclease protein with N-terminal Met at position -1 and Glu at position 1, where its Met has been cleaved and its Glu has been autocyclised. The method of the invention involves subjecting pET11d-rono(Gl.M2JL) plasmid DNA to two different site-directed mutations, each using overlapping PCR protocol. The method is useful for constructing an isolated nucleic acid encoding the ribonuclease. The present amino acid sequence represents the northern leopard frog rampirnase protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAW35125 to AAW35135 represent recombinant fusion proteins (rOnc) which are modifications of the RMsse Onconase (RTW) (nOnc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumnor cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nonc and also lower immunogenicity in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells.
                                                                                                                                                                                                                                                                                                                                      1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEFVKAICKGIIASKNVLTT 60
                                                                                                                                                                                                                                                                                                                                                                           QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
present invention relates to a new method of constructing isolated
                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytotoxic; onconase; nonc; immunofusion;
                                                                                                                                                                                                                                               Score 556; DB 5; Length 104;
Pred. No. 2.1e-59;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R. pipiens recombinant RNase ronc fusion protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wlodawer A;
                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US002588.
                                                                                                                                                                                                                                               96.2%;
96.2%;
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                                                                                                                                                                                                                                                                                            Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNase A; ribonuclease; cy
tumour cell growth; frog.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-435168/40.
                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                            Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rana pipiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW35126;
                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                 Query Match
Best Local 8
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Onconase, phamaceutical, protein, adenocarcinoma, treatment, cisplatin, melphalan, adriamycin, ovarian cancer, ovary.
 1 EDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pharmaceutical contg. Cisplatin, Melphalan or Adriamycin - active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in=vitro against OVČAR-3 human ovarian adrenocarcinoma cells.
                                                        SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                  61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                                           Ą.
                                                                                                                                                                                                                                                                                ONCONASE (pharmaceutical protein)
                                                                                                                                                         AAR47303 standard; protein; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 13; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93WO-US006357,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-00921180.
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 95.2
nes 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ardelt WJ;
                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ALFA-) ALFACELL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-065396/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mikulski SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                       WO9403197-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUL-1992;
                                                                                                                                                                                                                             25-MAR-2003
09-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                        17-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                   61
                                                                                                                                                                                            AAR47303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                      RESULT 14
AAR47303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The protein is derived from fertilised frogg eggs. It has an iso-
electric point of 9.5 - 10.5, a blocked N-terminal gp. and is free of
earbohydrates. It is active against certain cancer cells. The combination
of the protein and (z-1-p-dimethylaminoethoxyphenyl-1, 2-diphenyl-1-
butene) citrate salt (Tamoxifent) is much more bio- active than the
separate entities against human pancreatic ASPC-1 adenocarcinoma, and the
combination of protein and (10-13-4(-methyl piperazin-1-1/1)-propyl]-2-
trifluoromethylphenochiazine (Stelazine) is much more reactive than the
separate entities against human lung A-549 carcinoma. Activity has also
been shown against human sub- maxilliary epidermoid carcinoma A-253
cells, human ovarian adeno- carcinoma NIH-0VCAR-3 cells, human leukaemic
squamous car- cinoma HT-520 cells
                                                                                                                        0.9
                                                                                                                                                QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from fertilised eggs of Rana pipiens - active against cancer in combination with Tamoxifen or Stelazine (trifluoro-per-
                                                                                                                     QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                    Gaps
                                                                                    .,
                                               Score 556; DB 2; Length 379;
Pred. No. 1.1e-58;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.7%; Score 553; DB 2; Length 104; 95.2%; Pred. No. 5e-59;
                                                                                                                                                                                        SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                    SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGC 129
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                                                                                                                                                                                                                                                                                                                                                                                                                    Protein with activity against cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frog eggs; Tamoxifen; Stelazine; cancer.
                                                                                                                                                                                                                                                                                                             AAR12344 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Fig 2; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89US-00436141.
90US-00526314.
                                                 96.2%;
96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89US-00436141
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                          Query Match
Best Local Similarity 96.2
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mikulski SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ALFA-) ALFACELL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-178059/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
              Sequence 379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                   08-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1990;
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Ardelt

azine)

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o;
This pharmaceutical protein (ONCONASE) is used in the production of a bioactive pharmaceutical composition also comprising one of Cisplatin (cis-diamminedichloroplatinum), Melphalan, (4-[bis-(2-chloroethyl)amino]-L-phenylamine) or Adriamycin (Doxorubicin HCl). The composition has bioactivity in vitro against OVCAR-3 human ovarian adenocarcinoma cells. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                          09
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                                                                                                                                                                                                                                                                                        1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                 95.7%; Score 553; DB 2; Length 104; 95.2%; Pred. No. 5e-59;
                                                                                                                                                                                                                                                                                                                                                                                                        SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                            SEFYLSDCNVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW00736 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
22-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW00736
ID AAW0
XX
AC AAW0
XX
DT 25-M
DT 22-M
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9

1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT

Matches

Protein derived from frogs eggs.

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of Rana pipiens frogs eggs. This protein is used for trating tumours in humans. Especially this protein was active against human submaxillary epidermoid carcinoma A-253 cells, human ovarian adenocarcinoma NIH-OVCAR03 cells, human leukaemic HL-60 cells, human COLO 320 DM cells originally isolated from colon adenocarcinoma, human LOX melanoma and human lung squamous carcinoma HT-520 cells. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a protein which was prepared by homogenisation
                                                                                                                                                                                                                                                                                                                                                                                          New isolated Rana pipiens frog protein - useful for the treatment of
                          Rana pipiens; ovarian adenocarcinoma NIH-OVCAR03 cell; frog; egg; submaxillary epidermoid carcinoma A-253 cell; tumour; human; leukaemic Hi-60 cell; COLO 320 DM cell; colon adenocarcinoma; LOX melanoma; lung squamous carcinoma HT-520 cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.7%; Score 553; DB 2; Length 104; 95.2%; Pred. No. 5e-59; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                 88US-00178118.
89US-00436141.
92US-00814332.
                                                                                                                                                                                                       94US-00283970,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Col 8; 7pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.27
Matches 99, Conservative
                                                                                                                                                                                                                                                                                                 (ALFA-) ALFACELL CORP.
                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-442459/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 104 AA;
                                                                                                                                                                                                     01-AUG-1994;
                                                                                                                                                                                                                                                   13-NOV-1989;
03-FEB-1992;
                                                                                                           Rana pipiens
                                                                                                                                                                                                                                    06-APR-1988;
                                                                                                                                        US5559212-A.
                                                                                                                                                                                                                                                                                                                             Ardelt WJ;
                                                                                                                                                                                                                                                                                                                                                                                                              tumours
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Search completed: May 7, 2004, 21:38:26 Job time: 45.363 secs

SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCBNQAPVHFVGVGHC 104

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Sequence 1, Appli
                                                                           (without alignments)
445.066 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43,
Sequence 1, A
Sequence 1, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 63,
                                                                                                                     578
1 QDWLTFQKKHLTNTRDVDCN......TFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 1
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Sequence
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Sequence
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                                                               May 7, 2004, 21:28:45; Search time 12.0636 Seconds
                                                                                                                                                                                                                                                                                                   Issued Patents AA:*

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2: /cgm2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgm2_6/ptodata/2/iaa/6A_COMB.pep:*

5: /cgm2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

5: /cgm2_6/ptodata/2/iaa/pcafiles1.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-687-748-1
US-08-626-288-1
US-08-626-429-1
US-08-875-811-63
US-08-875-811-63
US-08-921-619-1
US-08-921-619-1
US-08-975-811-39
US-08-875-811-31
US-08-875-811-51
US-08-875-811-51
US-08-875-811-51
US-08-875-811-51
US-08-875-811-51
US-08-875-811-51
US-08-875-811-51
US-08-875-811-30
                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                   389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            OM protein - protein search, using sw model
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seq length: 200000000
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Match Length DB
                                                                                                           US-09-961-400-2
                                                                                                                                                     BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                     Scoring table:
                                                                                                                      Perfect score:
                                                                                                                                                                                                                               Minimum DB :
Maximum DB :
                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                  Sequence:
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		Š		5-2	7-95	RESULT 1 US-08-467-95
	ALIGNMENTS					
sequence 1, App.	US-09-223-118-1	m	114	35.4	204.5	45
	-09-223-118	m	114	35.6	205.5	44
4 (	US-09-223-118-4	m	114		7.	43
χÒ.	US-08-875-811-8	m	111	50.0	289	42
77.	1	N	111	50.0	289	41
m i	US-09-986-119-3	4	83	77.0	445	40
m i	US-09-071-672-3	4	83	77.0	445	39
Sequence 2, Appli	US-08-875-811-2	٣	83	77.0	445	38
22,	US-08-875-811-22	m	111	83.7	483.5	37
47,	US-08-875-811-47	ო	360	84.8	490	36
07	US-08-875-811-20	m	107	91.2	527	35
	US-08-875-811-53	m	365	93.8	542	34
45,	US-08-875-811-45	m	358	93.8	542	33
26,	US-08-875-811-26	٣	105	94.5	546	32
	US-08-875-811-24	m	105	94.5	546	31
7	-60-	4	104	94.8	548	30
7	-08-626-288-	4	104	94.8	548	29
7	1	4	104	94.8	548	28

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GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Ardelt Ph.D, Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.A.
STREET: P.O. Box E
CITY: Short Hills
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRIOR APPLICATION NUMBER: US 07/436,141
FILING DATE: 05-FEB-1992
FILING DATE: 05-FEB-1992
FILING DATE: 01-ABS-1992
APPLICATION NUMBER: US 07/814,332
FILING DATE: 01-ABS-1992
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-912-0442
TELEX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 500
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 201-912-9066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 07078-0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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Sequence Sequence

Sequence Seguence Sequence Sequence ó:

Gaps

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2; Indels

Length 104;

protein

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1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Youle, Richard
APPLICANT: Vosnamani, Veena
APPLICANT: Win Yon-Neng
APPLICANT: Win Yon-Neng
APPLICANT: Ardelt, Wojeiech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: Allows Production by Recombinant Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.2%; Score 556; DB 4; Length 104; 96.2%; Pred. No. 3.7e-60; Live 2; Mismatches 2; Indels
                                                                                                                                                                                   61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94105-1492

COMPUTER READABLE FORM:
MEDIUM TYPE: Rioppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,288
FILING DATE: No. 6649392 yet assigned
CLASSIFICATION: S30
ATTORNEY/AGENT INFORMATION:
NAME: Ran, David B.
                                 96.2%; Score 556; DB 4;
96.2%; Pred. No. 3.7e-60;
tive 2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Townsend and Townsend and Crew
One Market Plaza, Steuart Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 15280-267
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Townsend and Townsend
                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/08626288
; Patent No. 6649392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38,589
                             Query Match
Best Local Similarity 96.2°
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 104 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 96.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ran, David B. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
STREET: On
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                              RESULT 4
US-08-626-288-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-626-288-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
TITLE REFERENCE: 5013 US 019
CURRENT APPLICATION NUMBER: US/09/687,748
PRIOR APPLICATION NUMBER: 09/394,268
PRIOR FILING DATE: 1999-09-10
                                                                                                                                                                                                                                              1 QDWLTEQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
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                                                                                                                                                                                                                                                                        Sequence 1, Application US/09394268
Patent No. 6175003
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
TITLE OF INVENTION: MAKING THEM
TITLE OF INVENTION: MAKING THEM
CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ 1D NOS: 8
SOFTWARE PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKALCKGIIASKNVLTT
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                                                                                                                                                                                                                     0;
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                                                                                                                                                                       Score 558; DB 1; Length 104;
Pred. No. 2.1e-60;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 104;
                                                                                                                                                                                                                                                                                                                       61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                               61 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.2%; Score 556; DB 3; Lv 96.2%; Pred. No. 3.7e-60; live 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09687748
Patent No. 6423515
                                                                                                                  Oocyte
                                                                                                                                                                   96.5%;
                                   ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1 LENGTH: 104
                                                                                          ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: O
                                                                                                                                                                   Query Match
Best Local Similarity 96.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 96.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-687-748-1
MOLECULE TYPE:
                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104
                                                                                                                            US-08-467-955-2
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Two Embarcadero Center, Eighth Floor
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Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41,739
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 21-FEB-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Faris, Susan K. REGISTRATION NUMBER: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                      San Francisco
                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-875-811-43
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                                                                                   APPLICANT: Youle, Richard
APPLICANT: Vole, Richard
APPLICANT: Vasandani, Veena
APPLICANT: War, Yon-Neng
APPLICANT: Boix, Ester
APPLICANT: Ardelt, Wojeiech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: Allows Production by Recombinant Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.2%; Score 556; DB 4; Length 104; 96.2%; Pred. No. 3.7e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 63, Application US/08875811
Fatent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Roque, Lluis
APPLICANT: Mlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/095,429
                                                                                                                                                                                                                                                                                    E: Townsend and Townsend and Crew
One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Townsend and Townsend and Crew LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 15280-267 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/626,288
                      ; Sequence 1, Application US/09095429
; Patent No. 6649393
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ran, David B. REGISTRATION NUMBER: 38,589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 104 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
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Best Local Similarity
                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino STRANDEDNESS
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US-08-875-811-63
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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US-09-095-429-1
      US-09-095-429-1
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1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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Pred. No. 4.9e-60;
2; Mismatches 2; Indels
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APPLICANT: Rybak, Susanna M.
APPLICANT: Nowton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
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ADDRESSEE: Two Embarcadero Center, Eighth Floor CITY: San Francisco
CITY: San Francisco
CUTTY: USA
CONTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: USA 
COMPUTER READABLE FORM:
MEDIUM TYPE READABLE FORM:
MEDIUM TYPE ROOMPALINE
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORFWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6/011,800
APPLICATION NUMBER: US 6/011,800
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96.2%; Pred. No. ---
2; Mismatches
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1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIXSRPEPVKAJCKGIIASKNVLTT
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Patent No. 5595734
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D. Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brocklyn
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 553; DB 1; Length 104;
Pred. No. 8.5e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,619
FILING DATE: 19920728
CLASSIPETCATION 5AR.
APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Jay, MARK H.
      TELECOMMUNICATION INFORMATION:
TELERHONE: 718-625-0399
TELERX: No. 5529775 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: 708-625-0399
TELEX: NO. 5595734 Applicable INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
                                                                                                                                                                                                                                                                                                                                                                                                                                  95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.2<sup>5</sup>
Matches 99, Conservative
                                                                                                                                                                                      single
                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                 STRANDEDNESS: SI.
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 11202-0002
                                                                                                                                                                                                                                                                       ANTI-SENSE: N
FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                   US-08-283-971-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QDWLTFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 QDWLTFQXKHITINTRDVBCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08283971

Patent No. 5529775

GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanisław M.
TITEL OF INVENTION: PRARMACEUTICAL FOR TREATING TUMORS IN HUMANS NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 556; DB 3; Length 379;
Pred. No. 2e-59;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  015280-244100US
                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 06-APR-1988
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,180
FILING DATE: 30-UUL-1992
APPLICATION NUMBER: US 07/176,118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US 07/178,118
06-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5006 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 11202-0002
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                           NAME: Faris, Susan K.
REGISTRATION UNUBER: 41,739
REFERENCE/DOCKET UNUBER: 01526
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE GHARACTERISTICS:
LEMOTH: 379 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 96.2%;
Best Local Similarity 96.2%;
Matches 100; Conservative
19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-875-811-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-08-283-971-1
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Gaps ·,

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1 EDWLIFQKKHITUTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
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                                                                                                                                                                                                                                                                                         Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCBNQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                      ch 95.7%; Score 553; DB 1; Length 10 similarity 95.2%; Pred. No. 8.5e-60; 99; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/08891848

Batent No. 5955073

GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Nicholls, Peter J.
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REALABLE FORM:
COMPUTER REALABLE FORM:
MEDIUM TYPE: FIPOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/91,848
FILING DATE: US/08/91,848
FILING DATE: 22-SEP-1993
PRIOR APPLICATION NUMBER: US 08/125,462
FILING DATE: 22-SEP-1993
PRIOR APPLICATION NUMBER: US 08/014,082
FILING DATE: 04-FEB-1993
PRIOR APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-OCT-1991
PRIOR APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-APR-1990
ATTONEY/AGENT INPORMATION:
NUMBER: US 07/510,696
FILING DATE: 20-APR-1990
ATTONEY/AGENT INPORMATION:
NUMBER: US 07/510,696
FILING DATE: 21-APR-1990
ATTONEY/AGENT INPORMATION:
NUMBER: US 07/510,696
FILING DATE: 21-APR-1990
ATTONEY/AGENT INPORMATION:
NUMBER: US 07/510,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA: 21P: 94111-383.

ZIP: 94111-383.

ZIP: 94111-383.

MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32.762
REFERENCE/DOCKET NUMBER: 015280-110310US
TELECOMMUNICATION INFORMATION:
                                                                                            HYPOTHETICAL: NAMIL-SENSE: NERAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORIGINAL SOURCE: DEVELOPMENTAL STAGE: OOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                       single
                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 99; Conserva
TYPE: amino acid
STRANDEDNESS: sir
                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-891-848-13
                                                 TOPOLOGY:
                                                                                                                                                                                                                                               US-08-467-955-1
                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EDMLIFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                          1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08467955
Patent No. 5728805
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
IIILE OF INTATION:
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        95.7%; Score 553; DB 1; Length 104; 95.2%; Pred. No. 8.5e-60; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRICASTRICATION: 435
PRICASTRICATION DATA:
APPLICATION NUMBER: US 07/176,118
FILING DATE: 06-APR-1986
PRICA APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRICA APPLICATION NUMBER: US 07/814,332
PRICATION NUMBER: US 07/814,332
PRICATION NUMBER: US 07/814,332
PRICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: JAY, MATK H.
REFERENCE/DOCKET NUMBER: 27507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07078-0383
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Mark H. Jay, P.A. STREET: P.O. BOX E CITY: Short Hills STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
                                                                                                                                                                                                                           ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
     LENGTH: 104 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                           HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                              99; Conservative
                                                                                  . protein
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-08-467-955-1
                                                                                                                                                                                                                                                                              US-07-921-619-1
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2 EDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPBPVKAICKGIIASKNVLTT 61
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                                                                                                                                                1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QDWLIFQXXHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                          Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 355;
                                                                                                                                                                                                                                                                          61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                              SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
                95.7%; Score 553; DB 3; Length 10
95.2%; Pred. No. 8.6e-60;
ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     185-08-875-811-41
185equence 41, Application US/08875811
195equence 41, Application US/08875811
196equence 41, Application US/08875811
196equence 41, Application US/08875811
196equence 41, Application US/08875811
196equence 41, Application M.
196equence 41, Application US/08875811
196equence 41, Application US/0887511
196equence 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB.1998
CLASSIFICATION: 43.
RPICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB.1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB.1997
RAPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB.1996
ATTORNEY/AGENT INFORMATION:
NAME: FAILS, SUSAN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUWIRY: USA ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 553; DB 3;
Pred. No. 4.2e-59;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 015280-244100US
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ZIF: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

"WUTTER: IBM PC compatible
"""""M: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                  99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match >>>...
Best Local Similarity 95.28
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-875-811-41
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312
                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                Score 553; DB 2; Length 104;
Pred. No. 8.5e-60;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                      /label≈ Onc
/note= "Onconase from Rana pipiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-08-875-811-39
Sequence 39, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTONNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             015280~244100US
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFRENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.7%;
Best Local Similarity 95.2%;
Matches 99; Conservative 3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
LENGTH: 104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 105 amino acids
amino acid
                                                                                                                      MOLECULE TYPE: protein
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                                                                                                                                                                                                               LOCATION: 1..104
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                   FEATURE:
NAME/KEY: Protein
                             TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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Pred. No. 4.3e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Mlodwer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
              Sequence 51, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybac, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Modawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 CAMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 12-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FRAIS SUBAR K.
                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CITY: California COUNTRY: USA ZIP: 94111-3834
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41,739
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amino acid
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Best Local Similarity 95.2'
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Faris, Susan K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-875-811-51
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US-08-875-811-51
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US-08-875-811-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1
OTHER INFORMATION: /note= "Xaa = pyroglutamic acid"
                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
TLING DATE: 19-FEB.1998
CLASSIFICATION DATA:
FILING DATE: 19-FEB.1998
FILING APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 PCT/US97/02588
FILING DATE: 19-FEB.1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W5 60/011,800
FILING DATE: 21-FEB.1996
ATTONNEY/AGENT INFORMATION:
NAME: FAILS SUBBRE: 41,739
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELEDEDHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trademark) from Rana pipiens"
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Best Local Similarity 96.1%; Pred. No. 1.5e-59;
Matches 99; Conservative 2; Mismatches 2;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                : Two Embarcadero Center, Bighth Floor
San Francisco
California
                                                                                                                                      COUNTRY: USA
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note
OTHER INFORMATION: Trade
FEATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..104 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS:
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7, 2004, 21:40:43

Search completed: May 7 Job time: 13.0636 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

May 7, 2004, 21:30:40 ; Search time 5.25351 Seconds (without alignments) 1030.796 Million cell updates/sec Run on:

US-09-961-400-2 578 1 QDWLJFQKKHLINTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	rana	6 rana	rana				_	-			P00673 balaenopter		P04059 proechimys					P31347 oryctolagus			_	Q8hzq0 pan troglod					myoxı		P00674 equus cabal	P04060 hystrix cri	0	373 bos	P31346 sus scrofa
DI	RN30_RANPI	RNPO_RANCA	LECS_RANJA	RNPL_RANCA	RNP_IGUIG	RNP GALMU	ANGR MOUSE		ANGI BOVIN	RNP_MYOCO	RNP BALAC	ANGI MACMU	RNP PROGU	ANGI_MOUSE	RNPB_CAVPO	ANGI PAPHA	RNP_CHIBR	ANGI_RABIT	RNP_HYDHY	RNP_HIPAM	ANGI MIOTA	RNS4_PANTR	ANGI HUMAN	ANGI_PANTR	RNP PIG	RNP BOVIN	RNP MYOGL	RNS4 HUMAN	RNP HORSE	RNP HYSCR			ANGI_PIG
DB		H	Н	ч	Н	Н	н	н	Н	1	7	٦	н	Н	Н	М	Т	П				Н	٦	П							Н		Н
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% Query Match		50.5	49.4			22.7	22.6	22.6			21.6			20.7	20.6	20.5	20.2	20.1	20.1	σ		6	δ	6	9	19.4		٠	٠	•	19.2		19.1
Score	556	292	285.5	269.5	149	131	130.5	130.5	128	126	125	121.5	120	119.5	119	118.5	117	116	116	114	114	113.5	113	113	112	112	112	111.5	111	111	111	111	110.5
Result No.	I I	7	Э	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19		21	22	23	24	25	26	27	28	29	30	31	32	33

P97426 mus musculu Q29542 giraffa cam	Q8wn62 saguinus oe P87350 axis porcin	P80929 bos taurus P00678 cavia porce	P07847 aepyceros m	P00668 ancilocapra P00661 ovis aries	Q8wn60 saimiri sci	046529 saimiri sci	P00657 bubalus bub
ECP1_MOUSE RNBR_GIRCA	ANGI_SAGOE RNBR_AXIPR	ANG2_BOVIN RNPA_CAVPO	RNP AEPME	RNP_SHEEP	ANGI_SAISC	RNS6_SAISC	RNP_BUBBU
пп	п п		ı — 1		Н	Н	Н
155	146 151	123	124	124	146	150	124
19.1	19.0 19.0	18.9	18.9	18.9	18.9	18.8	18.7
110.5	110	109	109	109	109	108.5	108
3.4 3.5	36	886	4 0	4 4 1 2 7	43	44	4.5

### ALIGNMENTS

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CHARACTERIZATION.
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SEQUENCE
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          SON THE TENERS TO THE TENERS T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P11916; Q9PWR7;
01-0CT-1989 (Rel. 12, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Ribonuclease, occytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Egg;
MEDLINE-8729649; PubMed=3304421;
Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
Takayanagi G., Hakomori S.;
"Amino acid sequence of sialic acid binding lectin from frog (Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90165825, PubMed-9497370,
Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
"The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
Tissue distribution, cloning, purification, cytotoxicity, and active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rana catesbelana (Bull frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                                                                            ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liao Y.-D.;
"A pyrimidine-guanine sequence-specific ribonuclease from Rana
                                                                                                                                                                                                                                                                                                                            Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                                                                                                                                                                                                                                         Score 556; DB 1;
Pred. No. 8.7e-53;
2; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catesbeiana (bullfrog) oocytes.";
Nucleic Acids Res. 20:1371-1377(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        residues for RNase activity.";
J. Biol. Chem. 273:6395-6401(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92220613; PubMed=1373237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 26:2189-2194(1987).
                                                                                                                                                                                                                                                                                                                          96.2%;
96.2%;
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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48
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                                                                                                                                                                                                                                                                                          104 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8400;
                                   TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNPO RANCA
DISULFID
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                        ARDLINE-98437383; PubMed=9761686;

MEDLINE-98437383; PubMed=9761686;

MEDLINE-98437383; PubMed=9761686;

MEDLINE-98437383; PubMed=9761686;

The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeatana (bullfrog).";

J. Mol. Biol. 283:231-244(1998).

-! FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine residues with a 3'flanking guannine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization, and development of the frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00092; RNASE Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin. It is cytotoxic against several tumor cells. SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
TISSUE=Egg;
MEDILIBE-93192604; PubMed=8448385;
Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
Istayanagi Y., Hakomori S., Titani K.;
"Ribonuclease activity of sialic acid-binding lectin from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
8
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SIMILARITY: Belongs to the pancreatic ribonuclease family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIBONUCLEASE, OOCYTES.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14762 MW; A7D62594F7D16F0C CRC64;
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49.5%; Plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR, A27121; A27121.
PDB; 1BC4; Z8-OCT-98.
PDB; 1M07; Z1-JAN-03.
InterPro; IPR01427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                  catesbeiana eggs.";
Glycobiology 3:37-45(1993)
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133 AA;
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Best Local Similarity
Matches 55; Conserv
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IISSUE=Pancreas;
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P80287;
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RNP_IGUIG
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26
                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biochem. 108:139-143(1990).
-!- FUNCTION: The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin preferentially agglutinate a large variety of tumor cells, but it does not agglutinate a non-transformed cells and erythrocytes.
-!- SUBUNIT: Monomer.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family. PIR, JX0120, JX0120.
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ODWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                      23 QNWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKALCTGVI-NMN
QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H., Takayanagi Y., Titani K., "Amino acid sequence of a lectin from Japanese frog (Rana Japonica)
                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
10-CPT-1994 (Rel. 28, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Sialic acid-binding lectin (EC 3.1.27.-).
Shan alpointea (Japanese reddish frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLTTSEFYLSDC ---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                          104
                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 285.5; DB 1; Length 111;
; Pred. No. 8e-24;
19; Mismatches 35; Indels 7.
                                                                          VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPN001427; RNaseA.
Pfam; PF00074; TnaseA.
Probom; PR0000515; RNaseA.
SMART; SM00092; RNASe_PC; 1.
PROSTIE; PS00127; RNASE_PNNREATIC; 1.
PROSTIE; PS00127; RNASE_PNNCREATIC; 1.
Pytroliase; Muclease; Endonuclease; Sialic acid; Lectin; Pytrolidone carboxylic acid.
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12326 MW; FDEBDDF3834ED679 CRC64;
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SIMILARITY.
SIMILARITY.
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BY
BY
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                                                                                                                                                                                                              STANDARD;
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P14626;
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P18839;
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R. T. TAKAYA
D. R. RASEP;
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                                                                                                                                                                                                                                                                                                                                                  Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y., Okazaki T., Ohgi K., Irie M.; "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
01-APR-1990 (Rel. 14, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
02-FBB-2003 (Rel. 41, Last annotation update)
Ribonuclease, liver (EC 3.1.27.5).
Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Barrachia; Anura; Neobatrachia; Ranoidea; Rana.
NCBL_TAXID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iguana iguana (Common iguana).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Iguania, Iguanidae, Iguaninae, Iguana.
NCBI_TaxID=8517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ELSTISFKLNICIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U. Biochem. 106:729-735(1989).
-!- CATALYTIC ACTIVITY: Endomucleolytic cleavage to nucleoside phosphates and 3'-phosphooligonucleotides ending in C-P or with 2'.3'-cyclic phosphate intermediates.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao W., Beintema J.J., Hofsteenge J.; "The amino acid sequence of iguana (Iguana iguana) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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43.2%; Pred. No. 4.1e-22;
tive 19; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 AA
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HSSP; P1916; 1864.
HSSP; P1916; 1864.
PICAFPCO; 1PR001427; RNaseA.
PFCDOM; PD000535; RNaseA; 1.
PRODOM; P000092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94139745; PubMed=8307028;
                                                                                                                                                                                                                                                                                                         TISSUE=Liver;
MEDLINE=90130374; PubMed=2613682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111
12461 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 43.2
nes 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                        120 F 120
                                                                                                                                                                                                                                                                                                              98 F 98
                                                                                                                                                                                                                                                                                                                                                                                                          ANGR MOUSE
Q64438;
                     DISULFID
DISULFID
DISULFID
                                                             ACT_SITE
ACT_SITE
ACT_SITE
VARIANT
          DISULFID
                                                                                                                     SEQUENCE
                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                ANGR MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANGRP
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
          SHIFFFF
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                                                                                                                                                                                                                                                                                                                                                                                      1 QDWLTRQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPBPVKAIC--K 49
                                                                                                                                                                                                                                                                                                                                                                                                                ODWSSFONKHIDYPETSASNPNAYCDLMMORRNINPTKCKTRNTFVHASPSEIQQVCGSG 60
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beintema J.J., Neuteboom B., "Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amino acid sequences with those of two close relatives: capybara and cuis ribonuclease.";
CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
SUBCELLUIAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Mol. Evol. 19:145-152[1983].
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphate intermediates ending in C-P or U-P
with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galea musteloides (Cuis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Galea.
                                                                                                                                                            PROSITE; PRO127; RNASE PC; 1.
PROSITE; PS0127; RNASE PANCREATIC; 1.
PROSITE; PS0127; RNASE PANCREATIC; 1.
PYGROJASE; Nuclease; Bndonuclease; Pytrolidone carboxylic acid.
MOD RES
DISULFID 25 80 BY SIMILARITY.
DISULFID 39 91 BY SIMILARITY.
DISULFID 57 106 BY SIMILARITY.
ACT SITE 10 10 BY SIMILARITY.
ACT SITE 113 113 BY SIMILARITY.
ACT SITE 17 10 BY SIMILARITY.
ACT SITE 113 113 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                              50 GIIASKNVLTTSE-FYLSDC----NVTSRPCKYKLKKSTNTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                  16;
                                                   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family
                                                                                                                                                                                                                                                                                                                                     Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
                                                                                                                                                                                                                                                                                                                                                                 44; Indels
                                                                                                                                                                                                                                                                                                                                                 Pred. No. 3.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 AA
                                                                                                                                                                                                                                                                                                                                                              19; Mismatches
                                                                                                                                                                                                                                                                                                                                 25.8%; Score 149; 30.7%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00074; rnaseA; 1.

PRINTS; PR00794; RIBONUCLEASE.

ProDom; PD000535; RNaseA; 1.

SMART; SM00092; RNASE Pc; 1.

PROSITE; PS00127; RNASE PANCKEATIC; 1.

Hydrolase; Nuclease; Endonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87036770; PubMed=6571219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A00827; NRUI.
HSSP; P00656; 1SRN.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNASE1 OR RNS1
                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNP GALMU
P00680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEOUENCE
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RNP_GALMU
                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 QKNVPCKNGQINCYQSHSSMRIIDCRVISSSKXPNCSYRMIQAQKSIIVACEGTPSVPVH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : ||::|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 SKNV-----LTTSEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCEN--QAPVH 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129; TISSUE=Liver; MEDLINE=96079109; PubMed=8530072; Brown W.B., Nobile V., Subramanian V., Shapiro R.; The mouse angiogenin gene family: structures of an angiogenin-related protein gene and two pseudogenes."; Genomics 29:200-206(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LTFQKKHL-----TNTRDVDCNNIM---SINLFHCKDKNTFIYSRPEPVKAICKGIIA
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
BY SIMILARITY.
WY SOUTH STATEMENTY.
WISSING (IN 1/3 OF THE MOLECULES).
                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL,
ANGIOGENIN-RELATED PROTEIN.
PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                       Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                      34; Indels
                                                                                                                                                                                                                                                                                                                                            ; Score 131; DB 1;
; Pred. No. 3.1e-07;
18; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:104984; Magrp.
InterPro; IPR001427; RNaseA.
PEMM; PR00074; TRASEA, 1
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASE Po; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Signal, Hydrolase; Nuclease; Endonuclease;
Pyrrolidone carboxylic acid.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiogenin-related protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                             13870 MW;
                                                                                                                                                                                                                                                                                                                                            22.7%;
                                                                                                                                                                                                                                                                                                                                                                               30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U22519; AAA91367.1; -.
                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 30.6
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
       84
95
110
72
12
41
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                                                                                                                                                                                                                                                                             124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P03950; 1A4Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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us-09-961-400-2.rsp

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WEDUINE 1918422; PubMed=11919285;
A Zhang J., Rosenberg H.F.;
Thiversifying selection of the tumor-growth promoter angiogenin in primate evolution.";
Mol. Biol. Bvol. 19:438-445(2002).
Mol. Biol. Bvol. 19:438-445(2002).
C -1. PUNCTION: May function as a tRNA-specific ribonuclease that binds of a magiogenin is endocytosed and translocated to the nucleus, thereby promoting the endochelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity).
CC Hydrolyzing cellular tRNAs (By similarity).
CC -!- SUNCELIULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                          63 CKDVNTFIHDTKNNIKAICGKKGSPYGRNLRISKSRRQVITCTHKGRSPRPPCRYRASKG 122
                                                                                                                                              ---PCKYKLKKS 82
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD00035; NUMBER, SMRRIS; SMRRIS; SM0092; RNRSE PANCREATIC; 1.
FYGRIF; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Anglogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
24 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
                                                                                                                      7;
                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amortation update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                                                                                           Score 130.5; DB 1; Length 145; Pred. No. 4.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANGIOGENIN.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                      29; Indels
                                                                                                                                              30 CKDKNTFIYSRPEPVKAIC--KGIIASKNV-LTTSEFYLSDCNVTSR
                                                                       29A6EB814429C4AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                 Cercopithecus aethiops (Green monkey) (Grivet)
                                                                                                                                                                                                                                                                              146 AA
                                                                                                                     11; Mismatches
  SIMILARITY
                                               SIMILARITY
                       SIMILARITY
                                     SIMILARITY
                                                           SIMILARITY
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  BY
BY
BY
BY
BY
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InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                       16612 MW;
                                                                                                                                                                                                                   123 FRYIIIGCENGWPVHF 138
                                                                                              22.6%;
38.2%;
                                                                                                                                                                                            83 INTECVICENDAPVHF 98
                                                                                                                        29; Conservative
                                                                                                                                                                                                                                                                              STANDARD;
  37
64
137
104
115
 37
64
137
50
50
63
145 AA;
                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                      RNASES
                                                                                                                                                                                                                                                                              CERAE
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
                                               DISULFID
                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD RES
                                                                                                                                                                                                                                                                                         Q8WN66;
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5 TFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIC---KGIIASKNV-LTT 60
                                                                                                                                                                                                                                                                                                           53 TWRRRHLTSP------CKDINTFIHGNRHHIKAICGDENGNPYGENLRISK 97
                                                                                                                                                                                                                                   23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89065101; PubMed=3197838;
Maes P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A.;
"The complete amino acid sequence of bovine milk angiogenin.";
FEBS Lett. 241:41-45(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bond M.D., Vallee B.L.; ^{\prime} Isolation of bovine angiogenin using a placental ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.;
"Crystal structure of bovine angiogenin at 1.5-A resolution.";
Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
                                                                                                                                                                                     DB 1; Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR.
MEDLINE=96280645; PubMed=8688423;
Lequin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, sequencing, and expression of bovine angiogenin."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                   Indels
                                                                                                                                       27860112E85B8DF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       98 SPFQVTTCNLRGGSPRPPCQYRAIRGSRNIVVGCENGLPVH 138
                                                                                                                                                                                                                                                                                                                                                                          61 SEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVH 97
                                                                                                                                                                                                             Pred. No. 4.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANGI_BOVIN STANDARD; PRT; 148 AA. P10.152, Q.9GKP9; 10. Created) 28-FEB-2003 (Rel. 41, Last sequence update) 115-MAR-2004 (Rel. 43, Last annotation update) Anglogenin-1 precursor (EC 3.1.27.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bond M.D., Strydom D.J.;
"Amino acid sequence of bovine angiogenin.";
Biochemistry 28:6110-6113(1989).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                   17; Mismatches
                                                                                                                                                                                     22.6%; Score 130.5; 30.7%; Pred. No. 4.2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION, AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95224057; PubMed=7708754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89375344; PubMed=277575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89118214; PubMed=3064806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor binding assay.";
Biochemistry 27:6282-6287(1988).
37 BY
64 BY
138 BY
105 BY
116 BY
131 BY
1644 MW;
                                                                                                                                                                                                                                     31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
  37
64
138
50
63
81
146 AA;
                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 24-148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 24-148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rissue=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rissue=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chang S.-I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rissue=Milk;
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BOVIN
                                                                                                                                                                                                                                   Matches
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FQKKHL-----INTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 LCKNGQINCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FERQHMDSRGSPSTNPNYCNEMMKSRNMTQGRCKPVNTFVHEPLADVQAVC----PQKUV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TISEFYLSDCNVTSRP----CKYKLKKSINIFCVTCENQ--APVHF 98
                         MEDLINE=77065676; PubMed=999896;
van den Berg A., van den Hende-Timmer L., Beintema J.J.;
"Isolation, properties and primary structure of coypu and chinchilla pancreatic ribonuclease.";
Biochim. Biophys. Acta 453:400-409(1976).
-!- CARALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphate intermediates.
with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. J. 157:317-323 (1976).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2', 3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SINGLARITY: PRIORES.
-!- SIMILARITY: Pelongs to the pancreatic ribonuclease family.
HSSP; P00656; ISRN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emmens M., Welling G.W., Beintema J.J., Inthe amino acid sequence of pike-whale (lesser-rorgual) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Cetacea, Mysticeti,
                                                                                                                                                                                                  SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
RNASEL OR RNSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LINKED (GLCNAC. . .).
4EB924E52B445832 CRC64;
                                                                                                                                                                                                                                                                                                                                                            Endonuclease; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.8%; Score 126; DB 1; 29.9%; Pred. No. 1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
N-LINKED (GICNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.9%; Preu. ....
                                                                                                                                                                                                                               HSSP, P00656; ISRN.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RNSeA; 1.
PRODOM; P000055; RNASeA; 1.
SWART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANYREATIC; 1.
                                                                                                                                                                                  -!- TISSUE SPECIFICITY: Pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=76277855; PubMed=962870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14267 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Balaenopteridae; Balaenoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            95
110
72
12
411
34
                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Nuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                    PIR; A00822; NRCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=9767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribonuclease."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNP_BALAC
ID RNP_BALAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P00673;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 DEYCENMAKNRRLIRPCKDRNTFIHGNKNDIKAICE----DRNGQPYRGDLRISKSEFQI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
                  16 DVDCNNIMSTNLF--HCKDKNTFIYSRPEPVKAICKGIIASKN-----VLTTSEFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myocastor coypus (Coypu) (Nutria).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Hystricognathi, Myocastoridae,
"Solution structure of bovine angiogenin by 1H nuclear magnetic
                                                                                                                                                                                                         TISSUE SPECIFICITY: Serum and milk. SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16969 MW; B7999124CBB523DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein synthesis inhibitor; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 TICKHKGGSSRPPCRYGATEDSRVIVVGCENGLPVHF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE, PS00127; RNASE PANCREATIC, 1.
Hydrolase, Nuclease, Endonuclease, Angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.1%; Score 128; DB 1; 34.0%; Pred. No. 7.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 SDC---NVTSR-PCKYKLKKSTNTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANGIOGENIN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF135124; AAG47631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB; 1GIO; 07-DEC-96.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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148
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105
116
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64
                                                                                                                                                                                                                                                                                                                                                                                                                     PDB; 1AGI; 03-APR-96.
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63
81
148 AA;
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P00676;
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SEQUENCE.
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RESULT 10

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ACT_SITE
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                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P04059;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LIFQKKHLINIRDVD----CNNIMSINLF---HCKDKNIFIYSRPEPVKAICKGIIASK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 NVLCKNGRINCYESNSIMHIIDCRQIGSSKYPNCAYKISQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 MKFOROHMDSGNSPGNNPNYCNOMMARRKMTOGRCKPVNTFVHESLEDVKAVC----SOK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIG. Evol. 19:438-445 (2002).
FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVL------TISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang J., Rosenberg H.F.; "Diversifying selection of the tumor-growth promoter angiogenin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity). SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                           ; Score 125; DB 1; Length 124;
; Pred. No. 1.3e-06;
15; Mismatches 42; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase
                                                                                                                                                                                                                                                                                                                            .) (30%).
                                                                                                                                                                                                                                                                                                                                   LINKED (GLCNAC. . .) (3(
F57475459F697E20 CRC64;
                                                146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=21918422; PubMed=11919285;
                                                                                                                                                    40 84 84 85 110 95 12 12 41 119 E 76 14125 MW; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
                   Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    21.6%;
  InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                        28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primate evolution."
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08WN63;
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1D ANGI MACMU

1D 28-FEB-10  

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or send an email to license@isb-sib.ch)

InterPro; IPR001427; RNaseA. Pfam; PF00074; rnaseA; 1. PRINTS; PR00794; RIBONUCLEASE.

EMBL; AF441667; AAL61649.1;

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4
                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                              53 TMRRRHLTSP-------CKDINTFVHGNRHHITAICGDENGSPYGGNLRIST 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIC---KGIIASKNV-LTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proechimys guairae (Casiragua).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Hystricognathi, Echimyidae, Proechimys.
                                                                                                                                                                                                                                               23; Gaps
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endomuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
24
BY SIMILARITY.
                                                                                                                                                                                                                       DB 1; Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1986 (Rel. 03, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A)
                                                                                           PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                               17; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                        SPFQVTTCKLRGGSPRPPCQYRATRGSRNIVVGCENGLEVH 138
                                                                                                                                                                                              E39A89215DB2A2A4 CRC64;
                                                                                                                                                                                                                                                                                                                         97
                                                                                                                                                                                                                                                                                                                        61 SEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Nuclease; Endonuclease; Glycoprotein.
DISULEID 26 84 BY SIMILARITY.
DISULEID 40 95 BY SIMILARITY.
DISULEID 58 110 BY SIMILARITY.
DISULEID 65 72 BY SIMILARITY.
ACT SITE 12 BY SIMILARITY.
ACT SITE 14 41 BY SIMILARITY.
ACT—SITE 119 119 BY SIMILARITY.
                                                                                                                                                                                                                       Score 121.5; DB 1
Pred. No. 3.8e-06;
                                                                                                      SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1986 (Rel. 03, Created)
                                                                                                                                                                                               16301 MW;
                                                                                                                                                                                                                       21.0%;
28.7%;
                                                                                                                                                                                                                                                29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                     24
146
25
                                                                                                                    37
64
138
105
116
                                                                                                                                                                                              146 AA;
                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNASE1 OR RNS1
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CAVPO
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DISULFID
SEQUENCE
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
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RNPB_CAVPO
                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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MEDLINE=22386257; PubMed=12477932;

MEDLINE=22386257; PubMed=12477932;

MEDLINE=22386257; PubMed=12477932;

MA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Baha S.S., Loquellano N.A., Perters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

RA Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Schen E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

RH terfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R Human and mouse colNA sequences.", Annara M.A.;

R Human and mouse colNA sequences.", Annara M.A.;

R Human and mouse colNA sequences.", Annara M.A.;
                                                                                               6 FQKKHL-----INTRDVDCNNIM-SINLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
                                                                                                                        FOROHIDSSGSPSTNPNYCNAMMKSRNMTQERCKPVNTFVHEPLADVQAVC----FOKNV 63
                                                                                                                                                                     64 PCKNGQSNCYESTSNMHITDCRLTSNSKFPDCLYRTSQEEKSIIVACEGNPYVPUF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochim. Biophys. Acta 1162:177-186(1993).

-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds cotion on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and
                                                                                                                                                     -----LITSEFYLSDCNVTSR----PCKYKLKKSINTFCVTCENQ--APVHF 98
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Serum; MBDLNE-91192291; PubMed=8448182; Bond M.D., Strydom D.J., Vallee B.L.; brancherization and sequencing of rabbit, pig and mouse angiogenins: discernment of functionally important residues and
                                                                                                                                                                                                                                                                                                                          2
                                          Length 128;
                                                                                                                                                                                                                                                                                          01-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Anglogenin precursor (BC 3.1.27.-) (Ribonuclease 5) (RNase
                                                                      36; Indels
  34 N-LINKED (GLCNAC. . .).
14244 MW; 2DB58093A9D3C936 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bond M.D., Vallee B.L., "Isolation and sequencing of mouse angiogenin DNA."; Blochem. Biophys. Res. Commun. 171:988-995(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                          ; DB 1;
4.8e-06;
 N-LINKED (GLCNAC.
                                                       Pred. No. 4.8e. 8; Mismatches
                                                                                                                                                                                                                                                       145 AA.
                                         20.8%; Score 120; 29.9%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91025023; PubMed=2222458;
                                                                    18;
                                                                                                                                                                                                                                                                               01-MAY-1991 (Rel. 18, Created)
                                                                    Conservative
                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                   (Mouse)
34
128 AA;
                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                  musculus
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15-MAR-2004
                                                                 35;
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             SEQUENCE
                                                                                                                                                     58
 CARBOHYD
                                         Query Match
                                                       Local
                                                                   Matches
                                                                                                                                                                                                                        RESULT 14
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KHLTNTRDVD------CONIMSTNLF--HCKDKNTFIYSRPEPVKAIC--KGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 KFLTOHHDAKPKGRDDRYCERMMKRRSLTSPCKDVNTFIHGNKSNIKAICGANGSPYREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=77185023; PubMed=862624;
van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastra W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primary
malignant tissues. Abolishes protein synthesis by specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Guinea-pig pancreatic ribonucleases. Isolation, properties, primar structure and glycosidation.";
Eur. J. Biochem. 75:91-100(19.7).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cavia porcellūs (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                           SIMILARITY: Belongs to the pancreatic ribonuclease family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 V-LITSEFYLSDCNVTS----RPCKYKLKKSINIFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06944260BB764938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.7%; Score 119.5; 30.8%; Pred. No. 6.2
                                                                                                                                                                                                                                                                       send an email to license@isb~sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANGIOGENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                       hydrolyzing cellular tRNAs.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                EMBL; BC055355; AAH55355.1; -.
PIR; A35932; A35932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16228 MW;
                                                                                                                                                                                                                                                                                                                        EMBL; U22516; AAA91366.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:88022; Ang.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37
64
137
104
115
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64
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25
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Search completed: May 7, 2004, 21:53:03 Job time : 6.25351 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

May 7, 2004, 21:38:36; Search time 9.43686 Seconds (without alignments) 1060.090 Million cell updates/sec

Title: Perfect score:

US-09-961-400-2 578 1 QDWLTFQKKHLINTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ribonuclease-relat	ribonuclease-relat	ribonuclease-relat	pancreatic ribonuc		_				pancreatic ribonuc		pancreatic ribonuc		angiogenin - rabbi	pancreatic ribonuc	pancreatic ribonuc				pancreatic ribonuc	ribonuclease 4 (EC			pancreatic ribonuc	pancreatic-type ri	angiogenin - pig			pancreatic ribonuc
SUMMARIES	a a	A39035	A27121	JX0120	JX0085	841111	NRUI	A32474	NRCU	NRWHK	NRKS	A35932	NRGPB	NRCB	B43825	NRYY	NRHP	NRHUAG	NRBOB	NRPG	NRBO	I52489	S08549	NRHO	NRPQ	820066	A43825	JC6159	NRSH	NRPRH
	DB	0	7	Н	7	7	H	H	Н	ч	Н	Н	Н	H	Н	<b>,</b>	Н	Н	Н	-	Н	N	(1)	Н	Н	7	Н	7	Н	Н
	* Query Match Length	104	111	111	111	119	124	125	128	124	128	145	128	124	125	128	124	147	124	124	150	147	124	128	128	167	123	155	124	124
	% Query Match	95.7	50.0	σ	9	r)	22.7	(1	⊣	Ξ.	ö	0	0	20.5	0	20.1	σ	19.6		19.4	•	19.3		•			19.1			18.9
	Score	553	289	285.5	269.5	149	131	128	126	125	120	119.5	119	117	116	116	114	113	112	112	112	111.5	111	111	111	111	110.5	•	109	0
	Result No.	 	7	3	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26		28	29

~	pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc	ï		pancreatic ribonuc								
NRGPA	807141	NRWB	NRGN	NRGF	JC6160	NRDEO	NRCM	NRCMM	NRCMB	NROW2	NRHY	NRDER	NRDEN	NREKN	NRDEF
<del>, ,</del> ,	N	Н	Н	-	7		-	-	н	н	Н	Н	Н	Н	Н
		4	4	4	9	4	4	4	4	œ	4	4	4	24	24
124	124	12	17	12	15	12	12	12	12	12	12	12	12	1	-
18.9 124															
	18.9	18.7	18.7	18.5	18.3	18.2	18.2	18.2	18.2	18.2	18.0	17.8	17.8	17.8	17.6

## ALIGNMENTS

RESULT 1 A39035 ribonuclease-related anti-tumor protein - northern leopard frog (fragment) C;Species: Rana pipiens (northern leopard frog) C;Becies: Rana pipiens (northern leopard frog) C;Becies: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993 C;Accession: 339035 R;Ardelt, W.; Mikulski, S.M.; Shogen, K. J. Biol. Chem. 266, 245-251, 1991 A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl A;Reference number: A39035; MUID:91033131; PMID:1985896 A;Accession: A39035 A;Accession: A39035 A;Actus: preliminary A;Molecule type: protein A;Molecule type: protein A;Residues: 1-104 <ard> C;Superfamily: pancreatic ribonuclease</ard>	
Query Match 95.7%; Score 553; DB 2; Length 104; Best Local Similarity 95.2%; Pred. No. 1.1e-48; Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0; Qy 1 QDWLTPQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60  Db 1 EDWLTPQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60	

qq	:
λŏ	61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
4	

# g

A27121	ribonuclease-related sialic acid-binding lectin - bullfrog	C;Species: Rana catesbeiana (bullfrog)	C,Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993	
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RESULT

C;Accession: A27121
R;Titani, K; Takinada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanagi Biochemistry 26, 2189-2194, 1987
B;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A;Title: Amino acid sequence of sialic acid-binding lectin
A;Molecule type: Drotein
A;Molecule type: protein
A;Rotessidue: 1-111 crit>
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pancreatic ribonuclease

8; Gaps Query Match 50.0%; Score 289; DB 2; Length 111; Best Local Similarity 48.6%; Pred. No. 4.2e-22; Matches 54; Conservative 17; Mismatches 32; Indels

3;

1 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN

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guinea-pig: comparison of the
C;Species: Iguana iguana (common iguana)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: 841111
R;Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Bur. J. Bicchem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A;Reference number: 841111; MUID:94139745; PMID:8307028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Molecule type: protein

A/Residues: 1-124 <BEI>
A/Note: about one-third of the molecules lacked Ala-1

C/Comment: The cuis is a rodent belonging to the same subfamily as the guinea pig.
C/Superfamily: pancreatic ribonuclease
C/Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F/12,41,119/Active site: His, Lys, His #status predicted
F/26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 QKNVPCKNGQTNCYQSHSSMRITDCRVTSSSKYPNCSYRMTQAQKSIIVACEGTPSVPVH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---INTRDVDCNNIM---SINLFHCKDKNTFIYSRPEPVKAICKGIIA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKNV------LITSEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCEN--QAPVH 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreatic ribonuclease (EC 3.1.27.5) - cuis
NAIdernate names: RNase 1; RNase A.
C.Species: Galea musteloides (cuis)
C.Species: Galea musteloides (cuis)
C.Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 04-Oct-1996
C.Accession: A00827
M.O. Evol. 19, 145-152, 1983
A.Tille: Origin of the duplicated ribonuclease gene in guinea-pig: comparisc A;Reference number: A92957; MUID:87036770; PMID:6571219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    angiogenin [validated] - bovine
N.Alternate names: angiogenesis factor
N.Contains: ribonuclease (BC 3.1.27.-)
C.Species: Bos primigenius taurus (cattle)
C.Stecies: Scsp.1989 #sequence revision 25-Sep-1989 #text_change 15-Sep-2000
C.Accession: A32474; S02001; A30044; S48212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 MKEQRQHMDSDGHPDTNTN--YCNEMMVRRSMTQGRCKPVNTFVHEPLEAVQAVC----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QDWLTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAIC--K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ::|| |:|| |:|| GTHYEDNLYDSNESFBLYDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 GIIASKNVLTTSE-FYLSDC----NVTSRPCKYKLKKSTNTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                                                                                                                                                                                                                                                             Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;94/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                               44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Indels
                                                                                                                                                                                                                                                                                                                                                          25.8%; Score 149; DB 2; 30.7%; Pred. No. 5.5e-08; ive 19; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.7%; Score 131; DB 1; 30.6%; Pred. No. 3.7e-06; iive 18; Mismatches 34;
                                                                                                                                                                                                                     A;Status: preliminary
A;Moleoule type: protein
A;Residues: 1-119 <ZRA>
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 30.00.
These 37, Conservative
---TN
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: J0085
B;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
J; Biochem. 106, 729-735, 1989
A;Titla: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A;Reference number: JX0085; MUID:90130374; PMID:2613682
                                                                                                                                                                                                                                                                                                                           K.; Kawauchi, H.; Takayanagi,
                                                                                                                                                                                                                                                                                                                                                                                      eggs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribonuclease-related sialic acid-binding lectin - Japanese frog
C;Species: Rana japonica (Japanese frog)
C;Date: 10-Sep_1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                     A; Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) A; Reference number: JX0120; MUD:91035319; PMID:2229005
A; Rocession: JX0120; MUD:91035319; PMID:2229005
A; Rocession: JX0120; Protein
A; Rolecule type: protein
A; Residues: 1-111 < KAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ODWLTFOKKHLINTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: protein
A,Residues: 1-111 <NIT>
S,Superfamily: pancreatic ribonuclease
C;Keywords: hydrolase, pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10,35,104/Active site: His, Lys, His #status predicted
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                     60 VLSTTRFQLNTCTRTSITPRFCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 VLITSEFYLSDC---NVTSRPCKYKLKKSTNIFCVICENOAPVHFVGVGHC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 111;
                         --NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C'Superfamily: pancreatic ribonuclease
C'Reywords: lectin, pyroglutamic acid
F;1/Modified site: pyrroglutamic acid (Gln) #status exp
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                     R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta,
J. Blochem. 108, 139-143, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 285.5; DB 1;
Pred. No. 9.4e-22;
9; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.6%; Score 269.5; DB 2
llarity 43.2%; Pred. No. 3.8e-20;
Conservative 19; Mismatches 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pancreatic ribonuclease - common iguana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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1 Similarity 45.0%;
50; Conservative 19
                   VLTTSEFYLSDC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: egg
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Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                                                                                                      C; Accession: JX0120
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Best Local Simi
Matches 48;
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A. Accession: A. Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
Biochem. J. 157, 317-323, 1976
A. Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease. A. Reference number: A00818; MUID:76277855; PMID:962870
A. Accession: A00818
A. Accession: A00818
A. Accession: Accession: Accession and accession and accession and accession and accession accessio
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C.Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 30-Sep-1993
C.Jacession: A00821
C.Racession: A00821
R.Beintema, J.J.; Knol, G.; Martena, B.
B.Jochim. Biophys. Acta 705, 102-110, 1982
A.Fitle: The primary structures of pancreatic ribonucleases from African porcupine and A.Reference number: A90644; MUID:83000399; PMID:7115727
A.Accession: A00821
A.Molecule type: protein
A.Residues: 1-128 - ABIS -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQKKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --CNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:::|:
|FERQHMDSRGSPSTNPNYCNEMMKSRNMTQGRCKPVNTFVHEPLADVQAVC----FQKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --ITSEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 NVL------TISEFYLSDCNVISRP----CKYKLKKSINTFCVTCENQ--APVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCKNGQTNCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVHF
                                                                     C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
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                                                                                                                                                                                                                                                                                                                                                                                     Length 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                           21.8%; Score 126; DB 1;
29.9%; Pred. No. 1.2e-05;
ive 18; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pancreatic ribonuclease (EC 3.1.27.5) - minke whale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       casiragua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pancreatic ribonuclease (EC 3.1.27.5) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LTFQKKHLTNTRDVD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Conservative
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 35; Consery
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Best Local Similarity
Matches 34; Conserv
                                       A;Residues: 1-128 <VAN>
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A, Reference number: $68212; MUID: 95010071; PMID: 7925406
C, Function:
A, Description: hydrolyzes tRNA, induces vascularization of normal and malignant tissues C, Superfamily: pancreatic ribonuclease
C, Superfamily: pancreatic ribonuclease
C, Reywords: angiogenesis; hydrolase; nucleic acid degradation
F, 60-68/Region: receptor binding #status predicted
F, 1115/Active site: His, Lys, His #status predicted
F, 27-82, 40-93, 58-108/Disulfide bonds: #status experimental
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Nathernate names: RNase 1, RNase A
C; Alternate names: RNase 1, RNase A
C; Species: Myocastor coypus (nutria, coypu)
C; Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C; Date: 24-Apr-1984 A. van den Hende-Timmer, L.; Beintema, J.J.
B; Oshim. Blophys. Acta 453, 400-409, 1976
A; Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic A; Reference number: A30612; MUD:77065676; PMID:999896
A; Molecule type: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125 R; Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L. Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995
A; Title: Crystal structure of bovine angogenin at 1.5 Angstroms resolution. A; Reference number: A58315; MUID:95524057; PMID:7708754
B; Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y. Submitted to the Brookhaven Protein Data Bank, April 1996
A; Reference number: A65709; PDB:1GIO
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                                                                                                                                                                                                                                                                                                                                                                                               C.; Montreuil, J.; Spik, G.; Tartar,
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Lallemand, J.Y.
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A;Title: Solution structure of bovine angiogenin by (1)H nucl A;Reference number: A58821; MUID:96280645; PMID:8688423
A;Contents: annotation; conformation by (1)H-NMR R;Reisdorf, C.; Abergel, D.; Bontems, F.; Lallemand, J.Y.; DE Bur. J. Biochem. 224, 811-822, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Experimental source: milk R, Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L. submitted to the Brookhaven Protein Data Bank, January 1995 A; Reference number: A65065; PDB: 1AGI
R;Bond, M.D.; Strydom, D.J.
Biochemistry 28, 6110-6113, 1989
A;Title: Amino acid sequence of bovine angiogenin.
A;Reference number: A32474; MUID:89375344; PMID:2775757
A;Accession: A32474
A;Molecule type: protein
A;Molecule type: protein
A;Experimental source: plasma
B;Maes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spi)
FEBS Lett. 241, 41-45, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Title: The complete amino acid sequence of bovine mill
A.Reference number: S02001; MUD:89065101; PMID:3197838
A.Accession: S02001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 1-125 < MAE>
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Best Local Similarity
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61

98

Matches

à g à g and

7;

Gaps

30;

54

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CyAccession: A00820
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic A;Reference number: A90612; MUID:77065676; PMID:999896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 angiogenin - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Accession: 829833; B43825
B;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernm A;Reference number: 829833
A;Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernm A;Reference number: 829833
A;Accession: 829833
A;Accession: 829833
A;Accession: 529833
A;Accessio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pancreatic ribonuclease (EC 3.1.27.5) - Chinchilla brevicaudata (tentative sequence) N;Alternate names: RNase 1; RNase A C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata (C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNVLCKNGQINCYQSYSRMRIIDCRVISSSKFPNCSYRMSQAQKSIIVACEGDPYVPVHF 120
                                                                                                                                                                                                                                                                                                                       62 NVPCKNGQSNCYQSNSNMHITDCRLTSNSKYPNCSYRTSRENKGIIVACEGNPYVPVHF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                         --TISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF
                                                                                                                                                                                                                                                                   4 LTFQKKHL-----INTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAICKGIIAS
F:21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Note: a second component of chinchilla ribonuclease has 32-Asp C,Superfamily: pancreatic ribonuclease (5.Superfamily: pancreatic ribonuclease (5.Superfamily: pancreatic ribonuclease; second digestion; pancrease F;12,41,119/Active site: His, Lys, His status predicted F;12,41,119/Active site: His, Lys, His status predicted F;26-84,40-95,58-110,65-72/bisulfide bonds: #status predicted F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                  Length 128;
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26.9%; Pred. No. 9.6e-05;
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                                                                                                                                                                                            35; Indels
                                                                                                                      Score 119; DB 1;
Pred. No. 6.2e-05;
                                                                                                                  . Match
Local Similarity 28.3%; Pred. No. 6.2e
tes 34; Conservative 21; Mismatches
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Best Local Similarity
Matches 24, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 1-124 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A00820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 NV-
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                                                                                                                          Query Match
Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anglogenin precursor - mouse

N;Alternate names: angiogenesis factor
N;Alternate names: angiogenesis factor
N;Contcains: ribonuclease (EC 3.1.27.-)
C;Species: Mus musculus (house mouse)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C;Accession: A35932
R;Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A;Title: Isolation and sequencing of mouse angiogenin DNA.
A;Reference number: A35932
A;Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Residues: 1-145 -800N
A;Residues: 1-145 -800N
A;Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C;Genetics:
A;Introns: #status absent
C;Function:
A;Decentiation: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: pancreatic ribonuclease
C; Keywords: anglogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
C; Keywords: anglogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F; 25-145/Pomain: signal sequence #status predicted <MAT>
F; 25-146/Product: anglogenin #status predicted <MAT>
F; 25, Modified site: pyrrollidone carboxylic acid (Gln) (in mature form) #status predicted
F; 37, 64, 137/Active site: His, Lys, His #status predicted
F; 50-104, 63-115, 81-130/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  properties, primary structure
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                                                                                          7;
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                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNNIMSTNLF--HCKDKNTFIYSRPEPVKAIC--KGIIASKN 56
                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
NyAlternate names: RNase IB
C.Species: Cavia porcellus (guinea pig)
C.Species: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                      64 PCKNGQSNCYESTSNMHITDCRLISNSKFPDCLYRISQEEKSIIVACEGNPYVPUF 120
                                                                                                                                                                     6 FOKKHL-----INTRDVDCNNIM-SINLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV
                                                                                                                                                                                                                    98
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                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                          -----LTTSEFYLSDCNVTSR----PCKYKLKKSTNTFCVTCENQ--APVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 145;
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                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R, van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, Bur. J. Biochem. 75, 91-100, 1977
A, Title: Guinea pig pancreatic ribonucleases. Isolation, A, Reference number: A91247; MUID:77185023; PMID:862624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
                   20.8%; Score 120; DB 1; L. 29.9%; Pred. No. 5e-05; ive 18; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.7%; Score 119.5; DB 1
30.8%; Pred. No. 6.3e-05;
live 12; Mismatches 45
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Best Local Similarity 30.8'
Matches 33; Conservative
                                                                                                  35; Conservative
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A,Molecule type: protein
A,Residues: 1-128 <VAN>
                                                              Similarity
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                       Query Match
Best Local 8
                                                                                              Matches
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9

Gaps

28;

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3;

Gaps

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Pancratic ribonuclease (EC 3.1.27.5) - capybara
NyAlternate names: RNase 1; RNase A
C;Species: Hydrochaeris Nydrochaeris (capybara, carpincho)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 29-Oct-1999
C;Accession: A00824
R;Bebitnema, J.G.; Neuteboom, B.
G;Mol. Evol. 19, 145-152, 1983
A;Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the ami A;Reference number: A92957; MUID:87036770; PMID:6571219
A;Aocession: A00824
A;Aocession: A00824
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
30 CKDKNTFIYSRPEFVKAICK---GIIASKNV-LITSEFYLSDCNVTS----RPCKYKLKK 81
                                            4 LTFQKKHL-----TNTRDVDCNNIMSTNLF---HCKDKNTFIXSRPEPVKAIC-KGIIAS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 KNVLTT----SEFYLSDCNVTSR----PCKYKLKKSINTFCVTCENQ--APVHF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

20.1%; Score 116; DB 1; Length 128;
Best Local Similarity 27.8%; Pred. No. 0.00013;
Matches 32; Conservative 21; Mismatches 42; Indels ;
                                                                                                                                                                                                      99 GSRNIVIACENGLPVHF 115
                                                                                                                                          82 STNTFCVTCENQAPVHF 98
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Search completed: May 7, 2004, 21:54:53 Job time : 10.4369 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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using sw model - protein search, OM protein

7, 2004, 21:25:55 ; Search time 44.363 Seconds May Run on:

(without alignments)
662.376 Million cell updates/sec

US-09-961-400-4 Title: Perfect score:

579 1 QDWLTFQKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A Geneseq 29Jan04:\* Database

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* ..... Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

	Description	TO	Aav28866 Recombina			Recor		Recor		4	Н							·	_			Frod	Amino	7 Northe	~	D O	10
SUMMARIES	QI		AAY28866	AAY28869	AAY28865	AAY28867	AAY28879	AAY28870	AAY28871	AAW06544	AAW30301	AAB31666	ABG32650	AAW35126	AAW30302	AAR12344	AAR47303	AAW00736	AAW14065	AAW06543	AAW88233	AAY33322	AAB31667	ABG31617	AAW35123	AAY39400	AAW35125
	DB	H	0	(1	7	7	7	7	7	~	7	4	S	~	7	7	7	7	7	7	7	7	4	2	~	~	01
	Query Match Length		104	105	104	105	127	104	105	104	104	104	104		104	104	104	104	104	104	104	104	104	104	105	105	355
de	Query Match	1	98.6	•	•	98.3	98.3	97.4	97.4	94.8	•	94.5	94.5	94.5	94.3	94.0	94.0		94.0	94.0	94.0	94.0	94.0	94.0	•	94.0	94.0
	Score	1	571	571	569	569	269	564	564	549	547	547	547	547	546	544	544	544	544	544	544	544	544	544	544	544	544
	Result No.	1 1 1 1	H	7	m	4	Ŋ	9	7	œ ·	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aaw35130 R. pipien	2	Aaw35117 R. pipien	2	α,	2	p.	ρ	ρź	Ant	α	ß	ß	Aaw35131 R. ninien	2	ρ	ρ	ρ	ם ל	Frog
AAW35130	AAW35122	AAW35117	AAW35118	AAW35134	AAW35135	AAW35133	AAW35129	AAW35132	AAW18224	AAW35115	AAW35116	AAW35127	AAW35131	AAW35120	AAW35128	AAW35121	AAW35119	AAW88234	AAY33321
		7											~						~1
358	106	107	112	251	254	355	355	366	104	105	105	358	365	107	360	111	83	83	111
94.0	93.6	93.6	93.6	93.6	93.6	93.6	93.6	93.6	93.1	92.7	92.7	92.1	92.1	89.5	83.1	82.0	75.3	75.3	48.9
544	542	542	542	542	542	542	542	542	539	537	537	533	533	518	481	474.5	436	436	283
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

AAY28866

AAY28866 standard; protein; 104 AA

AAY28866; A X X B X X B X X B X X B X X B X X B X X B X

(first entry) 25-JAN-2000

Recombinant RaPLR1 Met23Leu amino acid sequence.

Recombinant Rana pipiens ribonuclease; RaPLR1 Met23Leu; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease.

Rana pipiens. Synthetic.

Location/Qualifiers Misc-difference

/note= "Wild type Met replaced with Leu"

W09950398-A2

07-0CT-1999.

99WO-US006641. 26-MAR-1999;

98US-0079751P. 27-MAR-1998; (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Newton DL; Rybak SM,

WPI; 1999-610847/52. N-PSDB; AAZ08125.

e.g. for New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.

Claim 34; Page 56; 71pp; English.

The present sequence is a recombinant Rana pipiens ribonuclease (RaPLRI) protein with Met23Leu. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerus B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant

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                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "(His)6 histidine tag attached to N-terminal Met"
ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cyclotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1; CD22; covalently bound; Li2 antibody; ligand binding moiety; RNase; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                1 QDWLTPQXKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                 QDWLTFQKKHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g
                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.
                                                                                                                                               Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Met not found in wild type RaPLR1"
                                                                                                                                                                                                                                                                                                   SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                              FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
                                                                                                                                              Score 571; DB 2; L. Pred. No. 5.8e-62; 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           AAY28869 standard; protein; 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; frog; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                               98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US006641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 59; 71pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-610847/52.
                                                                                                                                                             Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ08127.
                                                                                                                   Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rana pipiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4;
                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                           AAY28869;
                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                            AAY28869
                                                                                                                                                                                                                                                                                                                                                              RESULT
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cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rana pipiens liver ribonuclease, RaPLR1; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog; human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
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                                                                                                                                                                                                                                                                                           QDWLJFQKKHLJNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                           QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                       0
                                                                                                                                                                                    Length 105;
                                                                                                                                                                                                                                                                                                                                                                     SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                     FEFYLSDCNVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                  Score 571; DB 2;
Pred. No. 5.9e-62;
                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rana pipiens liver ribonuclease (RaPLR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 55; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY28865 standard; protein; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US006641.
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                                                                                                                                                                                  98.6%;
al Similarity 99.0%;
103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ08124
                                                                                                                                                  Sequence 105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana pipiens
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                                                                                                                                                                                      Query Match
                                                                                                                                                                                                       Local
                                                                                                                                                                                                                          Matches
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Sequence 104 AA;

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The present sequence is a recombinant Rana pipiens ribonuclease (RaPLRI) protein with Met at position 1. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding molety, which can be a LLZ antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                              Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                    QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                              1 ODWLTFOKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                  .;
   Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Met not found in wild type RaPLR1"
                                                                                                                                            FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                  1; Indels
 Score 569; DB 2;
Pred. No. 1e-61;
                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                   AAY28867 standard; protein; 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 34; Page 57; 71pp; English.
   98.3%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US006641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0079751P
                                                                                                                                                                                                                                                                                                                                   Recombinant Met (-1) RaPLR1
                                                                                                                                                                                                                                                                                                      (first entry)
                               Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-610847/52.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rana pipiens.
Synthetic.
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                                                                                            Н
                                                                                                                             61
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The present sequence is a Rana piplens Clone 5alb ribonuclease (RaPLRI). It is encoded by Clone 5alb cDNA obtained from Rana piplens liver mRNA library. It exhibits differences with Onconase (RTM) at amino acid residues 11, 20, 85 and 103. Carboxy terminal end of RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kapossi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methicnine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                             Rana pipiens ribonuclease Clone 5alb; RaPLR1; covalently bound; RNase; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase; Kaposi's Sarcoma; human chorionic gonadocrophin; hoc; cancer; recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
9
                               61
                    2 QDWLTFQKKGLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24. .127
/label= Rana_pipiens_Clone_5alb_ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 127;
                                                                                   62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 569; DB 2;
Pred. No. 1.3e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 23
/label= Signal_peptide
/note= "Putative"
                                                                                                                                                                                                                                                                                Rana pipiens Clone 5alb ribonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                               AAY28879 standard; protein; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 69; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US006641.
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98.1%;
                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ08136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    Rana pipiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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Gaps

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Score 569; DB 2; Length 105; Pred. No. 1e-61; 1; Mismatches 1; Indels

98.3**%**; 98.1**%**;

Best Local Similarity 98.1 Matches 102; Conservative

Query Match

104

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Recombinant Met(-1) Rana pipiens ribonuclease GlniSer; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
DWLIEGKKHLINIRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Met not found in wild type RaPLR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                                                                                      Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.
                                                                            EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                       EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
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                                                                                                                                                                                AAY28871 standard; protein; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US006641
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                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            autoimmune disease; RNase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ08129
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Rana pipiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                          62
                                                                                                                                                                                                                 AAY28871;
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                                      9
                                                                      83
                                                                                                                                                                                                                                                                                                                                                                         Recombinant Rana pipiens ribonuclease; RapLR1 Gln1Ser; covalently bound; Li2 antibody, 11gand binding moiecy; CD22; cancerous B cell; Frog; KapOs1's sarcoma; humar chorionic gonadotrophin; hGG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase;
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                                     QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                      QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
   Gaps
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   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 104;
                                                                                                       61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                            SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
   Indels
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Pred. No. 4.2e-61;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                        Recombinant RaPLR1 Gln1Ser amino acid seguence.
   1; Mismatches
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                                                                                                                                                                                                                                  AAY28870 standard; protein; 104
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ilarity 98.1%;
Conservative
                                                                                                                                                                                                                                                                                                       (first entry)
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-610847/52.
N-PSDB; AAZ08128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease.
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                                                                                                                                         84
                                                                                                                                                                                                                                                                   AAY28870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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   Matches
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                                                    The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Mer at position 1 and Gln2Ser. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD2 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an Neterminal methionine due to the presence of a signal peptide that is proteins to be fused in-frame with ligand binding moieties to form cyrotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DWLTEQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSREEPVKAICKGIIASKNVLTTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 564; DB 2; Length 105;
Pred. No. 4.3e-61;
1; Mismatches 1; Indels
Claim 34; Page 61; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               och 97.4%; al Similarity 98.1%; 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 101; Conserv
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Gaps

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DWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTF

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDWLTFQKKHVINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTF1YSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                        Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 549; DB 2; Length 104;
Pred. No. 2.9e-59;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104
                              EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                  EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                     Antitumour protein from Rana pipiens oocytes.
                                                                                                                                                       Lumour; chemotherapy; radiotherapy; frog.
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                                                                               AAW06544 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 104
                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 28; 45pp; English.
                                                                                                                                                                                                                               96WO-US008304
                                                                                                                                                                                                                                                95US-00467955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.8%;
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 94.2
Les 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant onc protein.
                                                                                                                                                                                                                                                                  (ALFA-) ALFACELL CORP
                                                                                                                                                                                                                                                                                                      WPI; 1997-043063/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW30301 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 104 AA;
                                                                                                                                                                         Rana pipiens
                                                                                                                                                                                          WO9639428-A1
                                                                                                                                                                                                                              03-JUN-1996;
                                                                                                                                                                                                                                                06-JUN-1995;
                                                                                                                   22-AUG-1997
                                                                                                                                                                                                             12-DEC-1996.
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                 62
                                                                                                 AAW06544;
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                                                                                                                                                                                                                                                                                    Ardelt
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ID AAW3
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AC AAW3
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DT 09-6
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                                                              RESULT 8
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- useful as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "this Gln is autocyclised to pyroglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QDWLTFQKKHITUTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant Onc protein with glutamine residue at position 1 - useful antitumour and antiviral agent, also as cell culture selection agent
Onc; oncanase; ribonuclease; frog; antitumour; pancreatic cancer; human immunodeficiency virus type-1; HIV1; replication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Ardelt W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a frog ribonuclease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 547; DB 2;
Pred. No. 5.2e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Boix E,
                                                                                                                                                                                                                                                                                                                                     SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frog; ribonuclease; ranpirnase; RNase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                     Wu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 28; 35pp; English
                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.5%;
94.2%;
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Best Local Similarity 94.2
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        Vasandani VM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
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                                                                                                                         WO9738112-A1
                                                                                                                                                                                                                                04-APR-1997;
                                                                           Rana pipiens
                                                                                                                                                                                                                                                                                    04-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                        Youle RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB31666;
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pipiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rana
                                                                                                                                                                                 Matches
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                                                                                                                                                     The present sequence represents a frog ribonuclease protein (ranpirnase) (RNase). The specification describes a synthetic ribonuclease protein, in which the addition of cysteine in the ribonuclease facilitates the chemical linking of a targetine molecule by the single reactive sulfhydryl group. The specification also describes a method for the production of rampirnase using DNA technology instead of processing biological material. The re-engineering of the protein molecule allows easier attachment to a targeting molecule thereby making it possible for mich, he more effective to a particular cell receptor where it
                                                                                        New nucleic acids encoding a ribonuclease (Rnase), useful for the precise targeting of Rnase to a predetermined cell receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Northern leopard frog; ranpirnase; site-directed mutation; ribonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Constructing isolated nucleic acid encoding ribonuclease, by subjecting desired recombinant plasmid DNA to different site-directed mutations to produce nucleic acid, using different polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                        QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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                                                                                                                                                                                                                                                                                                                         Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                         FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                       Score 547; DB 4;
Pred. No. 5.2e-59;
                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Northern leopard frog ranpirnase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG32650 standard; protein; 104
                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Col 5-6; 8pp; English
                                                                                                                                                                                                                                                                                                                       94.5%;
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                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 94.2
Best Local Similarity 94.2
Then 98; Conservative
                                                                                                                                                                                                                                                                    might be most effective
                                                                                                                           Claim 1; Col 5-6; 7pp;
             (ALFA-) ALFACELL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ALFA-) ALFACELL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-664633/71.
                                                               WPI; 2001-167808/17.
                                                                                                                                                                                                                                                                                               Sequence 104 AA;
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                                     Saxena
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            nucleic acid encoding ribonuclease protein with N-terminal Met at position 1 and Glu at position 1, where its Met has been cleaved and its Glu has been autocyclised. The method of the invention involves subjecting pETI1d-ronc(Q1,M21) plasmid DNA to two different site-directed mutations, each using overlapping PCR protocol. The method is useful for constructing an isolated mucleic acid encoding the ribonuclease. The present amino acid sequence represents the northern leopard frog rampirnase protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAW35125 to AAW35135 represent recombinant fusion proteins (ronc) which are modifications of the Rhase Onconase (RTW) (nonc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nonc and also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells.
invention relates to a new method of constructing isolated
                                                                                                                                                                                                                                                                                                                        1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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                                                                                                                                                                                                                                           Length 104;
                                                                                                                                                                                                                  Score 547; DB 5; Length Lu-
Pred. No. 5.2e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                      FEFYLSDCNVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R. pipiens recombinant RNase rOnc fusion protein 2.
                                                                                                                                                                                                                                                                               3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW35126 standard; protein; 379 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 68; 90pp; English.
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                                                                                                                                                                                                                                       94.5%;
94.2%;
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                                                                                                                                                                                                                                                                               98; Conservative
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tumour cell growth; frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Newton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-435168/40.
                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT94964.
                                                                                                                                                                                                   Sequence 104 AA;
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lower immunogenicity in humans

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0

Gaps

09

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This sequence represents a recombinant Onc protein comprising a 104 amino acid sequence having Gln at position 1. Onc, a ribonuclease from Rana pipiens occytes, is known as an antitumour agent (e.g. for treating pancreatic cancer) and inhibitor of human immunodeficiency virus type-1 replication. It can be used therapeutically or as a cell-culture selection agent, e.g. to identify gene therapy compositions able to inhibit tumour growth
                                                                                                               26 QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKALCKGIIASKNVLTT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant Onc protein with glutamine residue at position 1 - useful as antitumour and antiviral agent, also as cell culture selection agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "pyroglutamic acid; especially 2-pyrrolidone-5-carboxylic acid or 5-oxo-2-pyrrolidinecarboxylic acid"
                                                                                                QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                   Onc; oncanase; ribonuclease; frog; antitumour; pancreatic cancer; human immunodeficiency virus type-1; HIV1; replication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 546; DB 2; Length 104;
Pred. No. 6.8e-59;
3; Mismatches 3; Indels
                                         Length 379;
                                                                                                                                                                       SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 129
                                                                                                                                                    61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ardelt W;
                                         Score 547; DB 2;
Pred. No. 2.8e-58;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boix E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 28-29; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wu Υ,
                                                                                                                                                                                                                                                     AAW30302 standard; protein; 104
                                      94.5%;
94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US005675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-00626288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.3%;
                                                                                                                                                                                                                                                                                                             (first entry)
                       Query Match

Rest Local Similarity 94...

98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.2
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vasandani VM,
                                                                                                                                                                                                                                                                                                                                       Recombinant onc protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-512725/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 104 AA;
             Sequence 379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                            Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-1996;
                                                                                                                                                                                                                                                                                                           09-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9738112-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Youle RJ,
                                                                                                                                                                                 98
                                                                                                                                                                                                                                                                                 AAW30302;
                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                      XS
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The protein is derived from fertilised frogg eggs. It has an iso-electric point of 9.5 - 10.5, a blocked N-terminal gp. and is free of carbobydrates. It is active against certain cancer cells. The combination of the protein and (z-1-p-dimethylaminoethoxyphenyl-1, 2-diphenyl-1-butene) citrate salt (Tamoxifen) is much more bio-active than the separate entities against human pancreatic ASPO-1 adenocarcinoma, and the combination of protein and (10-[3-(4-methyl] piperazin-1-yl)-propyl]-2-trifluoromethylphenothiazine (Stelazine) is much more reactive than the separate entities against human lung A-549 carcinoma. Activity has also been shown against human sub- maxilliary epidermoid carcinoma A-253 cells, human colo 320 DM carcinoma NIH-OVCAR-3 cells, human leukaemic squamous car- cinoma HT-520 cells, human LOX melanoma and human lung aguamous car- cinoma HT-520 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from fertilised eggs of Rana pipiens - active against cancer in combination with Tamoxifen or Stelazine (trifluoro-per-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EDWLIFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 104;
                 61 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENOAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 544; DB 2;
Pred. No. 1.2e-58;
                                                                                                                                                                                                              Protein with activity against cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                             Frog eggs; Tamoxifen; Stelazine; cancer.
                                                                                                                 Ą
                                                                                                               AAR12344 standard; protein; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Fig 2; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                               89US-00436141.
                                                                                                                                                                                                                                                                                                                                                                                                             89US-00436141.
90US-00526314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.0%;
93.3%;
                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 93.3
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ardelt WJ, Mikulski SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ALFA-) ALFACELL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1991-178059/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 104 AA;
                                                                                                                                                                                                                                                                             Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                              13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-1990;
                                                                                                                                                                                                                                                                                                            WO9107435-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells, esp. azine).
                                                                                                                                                                               08-AUG-1991
                                                                                                                                                                                                                                                                                                                                             30-MAY-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New protein
                                                                                                                                              AAR12344;
                                                                               RESULT 14
                                                                                                 AAR12344
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AAR47303 standard; protein; 104 AA

RESULT 15
AAR47303
ID AAR47

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Gaps

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QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT

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This pharmaceutical protein (ONCONASE) is used in the production of a bloactive pharmaceutical composition also comprising one of Cisplatin (as-diamminedichloroplatinum), Melphalan, (4-bis-(2-chloroethyl)amino)-L-phenylamine) or Adriamycin (Doxorubicin HCl). The composition has bloactivity in vitro against OYCAR-3 human ovarian adenocarcinoma cells. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                 Onconase; phamaceutical; protein; adenocarcinoma; treatment; cisplatin; melphalan; adriamycin; ovarian cancer; ovary.
                                                                                                                                                                                                                                                                                                                                                                                           Pharmaceutical contg. Cisplatin, Melphalan or Adriamycin - active in-vitro against OVCAR-3 human ovarian adrenocarcinoma cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

Query Match

Best Local Similarity 93.3%; Pred. No. 1.2e-58;

Matches 97; Conservative 4; Mismatches 3; Indels
                                                                                     ONCONASE (pharmaceutical protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 13; 18pp; English.
                                                                                                                                                                                                                                                   93WO-US006357.
                                                                                                                                                                                                                                                                            92US-00921180.
                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                   Mikulski SM, Ardelt WJ;
                                                                                                                                                                                                                                                                                                         (ALFA-) ALFACELL CORP.
                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-065396/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 104 AA;
                                                                                                                                                                                         WO9403197-A1
                                                                                                                                                                                                                                                02-JUL-1993;
                                                                                                                                                                                                                                                                            30-JUL-1992;
                                         25-MAR-2003
09-SEP-1994
                                                                                                                                                                                                                   17-FEB-1994
                                                                                                                                                            Synthetic.
               AAR47303;
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Search completed: May 7, 2004, 21:38:26 Job time : 44.363 secs

0;

0; Gaps

61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104

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                                                                              7, 2004, 21:28:45; Search time 12.0636 Seconds (without alignments) 445.066 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 63,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39,
                                                                                                                                                    579
1 QDWLTFQKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 43,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1,
Sequence 1,
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-394-268-1
US-08-687-748-1
US-08-687-748-1
US-08-095-429-1
US-08-875-811-63
US-08-875-811-63
US-08-875-811-43
US-07-921-619-1
US-08-871-619-1
US-08-871-619-1
US-08-871-619-1
US-08-871-619-1
US-08-871-619-1
US-08-875-811-39
US-08-875-811-31
US-08-875-811-31
US-08-875-811-1
US-08-875-811-1
US-08-875-811-1
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US-08-875-811-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-08-875-811-30
                                                                                                                                                                                                                                      389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       - protein search, using sw model
                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                                                                                                                                       US-09-961-400-4
                                                                                                                                                                                             BLOSUM62
                                                                                   May
                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                     OM protein
                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                      Searched:
                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
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28         542         93.6         355         3         US-08-875-811-57         Sequence           29         542         93.6         355         3         US-08-875-811-64         Sequence           31         537         92.7         105         3         US-08-875-811-25         Sequence           32         537         92.7         105         3         US-08-875-811-26         Sequence           34         533         92.1         358         3         US-08-875-811-26         Sequence           34         533         92.1         365         3         US-08-875-811-26         Sequence           35         518         89.5         107         3         US-08-875-811-23         Sequence           36         89.5         107         3         US-08-875-811-20         Sequence           37         474.5         82.0         11         3         US-08-875-811-20         Sequence           38         436         75.3         83         3         US-08-875-811-20         Sequence           41         28         48.9         111         3         US-09-86-11-3         Sequence           43         75.3         83 </th <th>57, Appl</th> <th>64, Appl</th> <th></th> <th>24, Appl</th> <th>26, App]</th> <th>45,</th> <th>53,</th> <th>20,</th> <th>47,</th> <th>22,</th> <th>2, 1</th> <th>3, Appli</th> <th>3, Appli</th> <th>12, Appl</th> <th>8, Appli</th> <th>4, Appli</th> <th>2, Appli</th> <th>1, Appli</th>	57, Appl	64, Appl		24, Appl	26, App]	45,	53,	20,	47,	22,	2, 1	3, Appli	3, Appli	12, Appl	8, Appli	4, Appli	2, Appli	1, Appli
542 93.6 355 3 1542 93.6 355 3 542 93.6 355 3 537 92.7 105 3 533 92.1 355 3 153 92.1 355 3 153 92.1 355 3 153 92.1 355 3 153 92.1 355 3 153 92.1 355 3 153 92.1 355 3 153 92 92.1 355 92 92.1 355 92 92.1 355 92 92.1 3 159.5 34.3 114 3 1198.5 34.3 114 3 1198.5	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence									
542 93.6 542 93.6 542 93.6 537 92.7 533 92.1 533 92.1 44.5 88.1 436 75.3 436 75.3 436 75.3 283 48.9 211.5 34.5 199.5 34.3	US-08-875-811-57	US-08-875-811-64	US-08-875-811-55	US-08-875-811-24	US-08-875-811-26	US-08-875-811-45	US-08-875-811-53	US-08-875-811-20	US-08-875-811-47	US-08-875-811-22	US-08-875-811-2	US-09-071-672-3	US-09-986-119-3	US-08-891-848-12	US-08-875-811-8	US-09-223-118-4	- 1	US-09-223-118-1
542 93.6 542 93.6 542 93.6 537 92.7 533 92.1 533 92.1 44.5 88.1 436 75.3 436 75.3 436 75.3 283 48.9 211.5 34.5 199.5 34.3	m	ო	ო	m	m	٣	m	m	m	ო	٣	4	4	~	٣	ო	ო	٣
542 542 542 537 533 633 643 644.5 436 436 436 436 283 211.5 199.5	355	355	366	105	105	358	365	107	360	111	83	83	83	111	111	114	114	114
4 22.1	93.6	93.6	93.6	92.7	92.7	92.1	92.1	89.5	83.1	82.0	75.3	75.3	75.3	48.9	48.9	36.5	34.5	34.3
8 2 2 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	542	542	542	537	537	533	533	518	481	474.5	436	436	436	283	283	211.5	199.5	198.5
	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Actalt Ph.D, Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-NUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/467,955
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           Sequence 2, Application US/08467955
Patent No. 5728805
                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.A.
STREET: P.O. BOX E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
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REGISTRATION NUMBER: 27507
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CITY: Short Hills
STATE: New Jersey
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                          07078-0383
                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                             COUNTRY:
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US-08-467-955-2
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Query Match
Best Local Similarity 94.2%
....hes 98; Conservative
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Patent No. 6423515
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REFERENCE: 5013 US 0109/687,748
CURRENT FILING DAFE: 2000-10-14
PRIOR APPLICATION NUMBER: 09/394,268
PRIOR FILING DATE: 1999-09-10
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APPLICANT: SAXEDA, Shailendra K
APPLICANT: SAXEDA, Shailendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
TITLE OF INVENTION: MAKING THEM
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
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Pred. No. 1.4e-59;
3; Mismatches 3;
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Patent No. 6175003
                                                                                            ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Oocyte
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94.2%;
                                                             N-terminal
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Best Local Similarity 94.2<sup>3</sup>
Matches 98, Conservative
protein
N
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ORGANISM: Rana pipiens
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US-09-687-748-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
                                                                                                                                                                                    Best_Local Similarity
Matches 98; Conserv
                                          ANTI-SENSE: N
FRAGMENT TYPE: 1
ORIGINAL SOURCE:
       MOLECULE TYPE: HYPOTHETICAL:
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LENGTH: 104
TYPE: PRT
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US-09-394-268-1
                                                                                                                                  US-08-467-955-2
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US-09-687-748-1
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                                                      Gaps
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APPLICANT: Wa. Yon-Neng
APPLICANT: Wu, Yon-Neng
APPLICANT: Boix, Ester
APPLICANT: Ardelt, Wojeiech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: Allows Production by Recombinant Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
  Score 547; DB 4; Length 104;
Pred. No. 1.4e-59;
3; Mismatches 3; Indels
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Pred. No. 1.4e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,288
FILING DATE: No. 6649392 yet assigned
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ran, DAVIA B.
REGISTRATION NUMBER: 38,589
REFERENCE/DOCKET NUMBER: 15280-267
TELECOMMUNICATION INFORMATION:
MEDICOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco
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94.5%;
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94.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-626-288-1
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APPLICANT: Youle,
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Best Local Similarity
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Two Embarcadero Center, Eighth Floor
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TELEPHONE: (415) 576-0200
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INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 94.2
Matches 98; Conservative
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                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                     San Francisco
California
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STATE:
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       Sequence 1, Application US/09095429
Patent No. 6649393
GENERAL INFORMATION:
APPLICANT: Vasandani, Veena
APPLICANT: Wa. Yon-Neng
APPLICANT: Wa. Yon-Neng
APPLICANT: Maidt, Wojeiech
ITILE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
ITILE OF INVENTION: A Mutant Romm of Cytotoxic Protein Which
ITILE OF INVENTION: A Mutant Romm of Cytotoxic Protein Which
ITILE OF INVENTION: Allows Production by Recombinant Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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Fatent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rydak, Susanna M.
APPLICANT: Boque, Lluis
APPLICANT: Modawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
VUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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STATE: California
COUNTRY: USA
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APPLICATION NUMBER: US/09/095,429
                                                                                                                                                                                                                                                                                         Townsend and Townsend and Crew
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NAME: Ran, David B.
REGISTRATION NUMBER: 38,589
REFERENCE/DOCKET NUMBER: 15280-267
TELECOMMUNICATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,288
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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 98; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                         ADDRESSEE:
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26 QDWLTFQXKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 85
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APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Wlodawer, Alexander
ITITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENOAPVHFVGVGSC 129
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                                                                             SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTONNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
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94.2%; Pred. No. 1.9e-59;
iive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   015280-244100US
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 43, Application US/08875811
Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01.
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1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
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Patent No. 5595734
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
94.0%; Score 544; DB 1;
Best Local Similarity 93.3%; Pred. No. 3.3e-59;
Matches 97; Conservative 4; Mismatches 3
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SOFTWA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELEXX: NO. 5529775 Applicable
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: No. 559734 Applicable INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
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REGISTRATION NUMBER: 27507
                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: E
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TELEPHONE: 718-022
                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
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US-07-921-619-1
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Patent No. 5259773
GENERAL INFORMATION:
APPLICANT: Arcelt Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.5%; Score 547; DB 3; Length 379; 94.2%; Pred. No. 7.7e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 129
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STREET: P.O. Box 020083, General Post Office CITY: Brooklyn
STATE: New York
COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                    015280-244100US
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                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
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CLASAFIRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,180
FILING DATE: 30-001-1992
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
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FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5006 US
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                                                                                                                                                                                                                                                                                            NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01528
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-FEB-1998
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Best Local Similarity 94.2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / MOLECULE TYPE: protein US-08-875-811-43
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1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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Patent No. 5728805
GENERAL INFORMATION:
APPLICANT: Arcelt Ph.D, Wojciech J.
TILLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: P.O. BOX E CITY: Short Hills
STREET P.O. BOX E CITY: Short Hills
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5007 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REPERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                          ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 201-912-9066
TELEFAX: 201-912-0442
LENGTH: 104 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                              FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                        97; Conservative
                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                     linear
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                                                                                                                                        ANTI-SENSE: N
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US-08-467-955-1
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APPLICANT: Rybak, Richard J.
APPLICANT: Newton. Dianne L.
APPLICANT: Newton. Dianne L.
APPLICANT: Nicholls, Peter J.
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
NUMBER OF SEQUENCES:
TOWNSENDEWE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                           Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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APPLICATION NUMBER: US/08/891,848
FILING DATE: No. 595073 yet assigned CLASSIFICATION NUMBER: US/08/891,848
FILING APPLICATION DATE: US/08/891,848
FILING APPLICATION DATE: US/08/125,462
PRICTARY APPLICATION NUMBER: US/08/125,462
FILING DATE: 22-SEP-1993
PRIOR APPLICATION NUMBER: US/08/14,082
FILING DATE: 04-FEB-1993
PRIOR APPLICATION NUMBER: US/07/779,195
FILING DATE: 22-OCT-1991
                                                                                                                                                                                                                                                         94.0%; Score 544; DB 1;
93.3%; Pred. No. 3.3e-59;
tive 4; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32.772
REFERENCE/DOCKET NUMBER: 015280-110310US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 07/510,696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/08891848
Patent No. 5955073
GENERAL INFORMATION:
                                                           MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SORGE:
ORIGINAL SORGE:
DEVELOPMENTAL STAGE: OCCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 576-0200
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FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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OR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                    single
                                      linear
                                                                                                                                                                                                                                                                                  Best Local Similarity
amino acid
                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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INFORMATION FOR
                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-891-848-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                US-08-467-955-1
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                                                                                                                                                                                                                                                                                                       Matches
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ADDRESSEE:
                                  SEQ ID NO 2
LENGTH: 104
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US-08-626-288-2
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SOFTWARE:
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Patent No. 6423515
GAUGHEAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REPREMENT: 1031 US 01
CURRENT APPLICATION NUMBER: US/09/687,748
CURRENT FILING DATE: 2000-10-14
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QDWLTPQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 94.0%; Score 544; DB 2; Length 104; Best Local Similarity 93.3%; Pred. No. 3.3e-59; Matches 97; Conservative 4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                         /label= Onc
/note= "Onconase from Rana pipiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-394-268-2; Sequence 2, Application US/09394268; Patent No. 6175003
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Best Local Similarity 94.2'
Matches 98; Conservative
                                                                                                                           MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                   CTHER INFORMATION: /. US-08-891-848-13
                                                                                                                                                                                            NAME/KEY: Protein
               TYPE: amino acid STRANDEDNESS:
                                                                                            linear
                                                                                        TOPOLOGY:
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LENGTH: 104
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US-09-687-748-2
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1 QDWLTFQKKHITNTR5VDCDNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
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                                                                                                                                                                                                                                                                                          Gaps
                                                                                                             FEATURE: OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at OTHER INFORMATION: position 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Youle, Richard
APPLICANT: Vasandani, Veena
APPLICANT: Wu, Yon-Neng
APPLICANT: Wu, Yon-Neng
APPLICANT: Boix, Ester
APPLICANT: Ardell, Wojelech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: Allows Production by Recombinant Methods
                                                                                                                                                                                                                                     94.0%; Score 544; DB 4; Length 104; 94.2%; Pred. No. 3.3e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "OTHER"
/note= "xaa = pyroglutamic acid
(2-pyrrolidone-5-carboxylic acid or
5-oxo-2-pyrrolidinecarboxylic acid)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SEFYLSDCNVTCRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                              61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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One Market Plaza, Steuart Street Tower
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                                                                                                                                                                                                                                                                                     2; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,286
FILING DATE: No. 6649392 yet assigned
ACLASSIFFORMION: 530
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; Patent No. 6649392
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Ran, David B.
REGISTRATION NUMBER: 38,589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
PatentIn Ver. 2.0
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Matches 98; Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                                                                           2 DWLTFQKKHITNTRDVDCDNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
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APPLICANT: Vasandani, Veena
APPLICANT: Vasandani, Veena
APPLICANT: Wasandani, Veena
APPLICANT: Wasandani, Veena
APPLICANT: Ardelt, Worleisech
APPLICANT: Ardelt, Worleisech
APPLICANT: Ardelt, Worleisech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: Allows Production by Recombinant Methods
CORRESPONDENCE: January Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
                                   Query Match
94.0%; Score 544; DB 4; Length 104;
Best Local Similarity 95.1%; Pred. No. 3.3e-59;
Matches 98; Conservative 2; Mismatches 3; Indels
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94.0%; Score 544; DB 4; Length 104;
Best Local Similarity 95.1%; Pred. No. 3.3e-59;
Matches 98; Conservative 2; Mismatches 3; Indels
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OTHER INFORMATION: /note= "Xaa = pyroglutamic acid
OTHER INFORMATION: (2-pyrrolidone-5-carboxylic acid or OTHER INFORMATION: 5-oxo-2-pyrrolidinecarboxylic acid):
                                                                                                                                                                                                    62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                     62 EFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: BEN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/095,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,288
                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-095-429-2
; Sequence 2, Application US/09095429
; Betent No. 6649393
; GENERAL INFORMATION:
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STATE: California
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US-08-626-288-2
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865.070 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1140673 seqs, 277566755 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                             OM protein - protein search, using sw model
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seq length: 2000000000
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Perfect score:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Appl Appl Appli Appli Appli Appli Appli Appli Appli Appli Appli Sequence 4, Sequence 8, Sequence 9, Sequence 9, Sequence 8, Description Sequence ( Sequence Sequence Sequence Sequence Sequence Sequence US-09-948-391A-4 US-09-961-400-4 US-09-961-400-9 US-09-961-400-9 US-09-961-391A-9 US-09-948-391A-9 US-09-961-400-2 US-09-961-400-6 US-09-961-400-6 US-09-961-400-28 US-09-961-400-28 US-09-961-400-11 US-09-961-400-11 US-09-961-400-11 US-09-961-400-11 US-09-961-400-11 US-09-961-400-11 SUMMARIES 0000000000000000 DB Query Match Length 100.0 Score Result 

	3, Ag 3, 7 19, 19, 21,	22, 15, 15, 17,	19, 24, 24, 26,	Sequence 89, Appl Sequence 139, Appl Sequence 13, Appl Sequence 103, Appl Sequence 8, Appl Sequence 8, Appl Sequence 6, Appl Sequence 2, Appli Sequence 2, Appli
10 US-09-948-391A-2 14 US-10-153-882-2 9 US-09-986-119-1 10 US-09-918-887-1 12 US-10-461-713-53	9 US-09-986-119-3 10 US-09-918-887-3 10 US-09-961-400-19 10 US-09-961-400-21 10 US-09-961-400-21		10 US-09-948-391A-19 10 US-09-948-391A-24 10 US-09-961-400-24 10 US-09-968-391A-26 10 US-09-961-400-26 10 US-09-968-391A-17	5 55
104 105 104 104	83 110 111 111	110	110 1110 1111 1111	112 112 122 124 144 147 147
96.7 94.5 93.6 93.6	75.3 75.3 747.8 74.8	47.8 47.8 47.6 47.6	4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6	2455 2000 2000 2000 118.7 18.3
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## ALIGNMENTS

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OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens OTHER INFORMATION: ribonuclease with Met23Leu substitution OTHER INFORMATION: (recombinant RaPLR1 Met23Leu)
                                                                                                                                                                                APPLICANT: Newton, Dianne L. APPLICANT: The United States of America APPLICANT: The United States of America APPLICANT: Sa represented by The Secretary of the APPLICANT: Department of Health and Human Services FITLE OF INVENTION: Recombinant Anti-Tumor RNase FITERE REFERENCE: 015290-343110US CURRENT APPLICATION NUMBER: US/09/948,391A CURRENT FILING DATE: 2002-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1938-03-27
PRIOR FILING DATE: 1938-03-27
PRIOR PELING DATE: 1939-03-26
PRIOR FILING DATE: 1939-03-26
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
LENGTH: 104
TYPE: PRT
ORGANISM: Artificial Sequence
                                                        Sequence 4, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
                                                                                                                                                            APPLICANT: Rybak, Susanna M.
RESULT 1
US-09-948-391A-4
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9 QDMLTFQKKGLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT Н

0;

0; Gaps

Length 104; Indels

100.0%; Score 579; DB 10; 100.0%; Pred. No. 1.4e-59; ive 0; Mismatches 0;

Query Match
Best Local Similarity 100.0
Matches 104; Conservative

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US-09-948-391A-8
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US-09-961-400-9
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Publication No. US20030124131A1

GENERAL INFORMATION:
APPLICANT: NEWLOW.
TITLE OF INVENTION:
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/961,400

FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: 09/622,613

FILE REPLICATION NUMBER: 09/622,613

FRICK APPLICATION NUMBER: 09/622,613

FRICK APPLICATION NUMBER: 09/622,613

FRICK APPLICATION NUMBER: 00/079,751

FRICK APPLICATION NUMBER: 60/079,751

FRICK APPLICATION NUMBER: 60/079,751

FRICK APPLICATION NUMBER: 60/079,751

FRICK APPLICATION NUMBER: 60/079,751

FRICK APPLICATION NUMBER: 2010-08-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VOY: 2.1

SEQ ID NO 8

LENGTH: 105
                                                                                                                                                                                            Sequence 4, Application US/09961400

Publication No. US20030124131A1

GENERAL INRORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: MENTON:
INMUNICONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: IMMUNCCNJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE OF INVENTION: CELLS
FILE OF INVENTION: CELLS
CURRENT APPLICATION UNMER: 09/62,613
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 1099-03-26
FRIOR PAPLICATION NUMBER: 60/079,751
FRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOSTWARE: PATCH IN UNER: 2010-08-25
SOSTWARE: PATCH OF THE SEQ ID NOS: 43
SOSTWARE: PATCH IN UNER: 2010-08-26
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QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
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                                            FEFYLSDCNVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
                                                                        FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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100.0%; Score 579; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.4e-59;
Matches 104; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Rana pipiens
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; ORGANISM: Rana pipiens
US-09-961-400-8
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US-09-961-400-8
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Sequence 9, Application US/09961400

Sequence 9, Application US/09961400

Bublication No. US20030124131A1

GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: REFERENCE, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: UMBARS. US/09/961,400

FILE REFERENCE: 016733/1059

CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613

PRIOR FILING DATE: 2000-08-17

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.1
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                                                                                                                QDWLTFQKKHLTNTRDVDCNN1LSTNLFHCKDKNTF1YSRPEPVKA1CKG11ASKNVLTT
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        Length 105;
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  Score 575; DB 10; Length 1
Pred. No. 4.2e-59;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                      FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                   61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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APPLICANT: The United States of America
APPLICANT: a represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.6%; Score 571; DB 10; 99.0%; Pred. No. 1.3e-58;
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR PLING DATE: 1999-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
Query Match
Best Local Similarity 99.0%;
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.0
Matches 103; Conservative
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us-09-961-400-4.rapb

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Sequence 2, Application US/09961400

Publication No. US20030124131A1

GENERAL INFORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

TITLE OF INVENTION: LIMMUNCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: LELLS

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: LOGICS

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT APPLICATION NUMBER: US/09/25

PRIOR FILING DATE: 1200-08-17

PRIOR PILING DATE: 12099-03-26

PRIOR APPLICATION NUMBER: GO/79,751

PRIOR FILING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-26

SEQ ID NO 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.3%; Score 569; DB 10; Length 104; 98.1%; Pred. No. 2.1e-58;
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APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REPERENCE: 015280-343110US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR RILING DATE: 1999-03-26
PRIOR RILING DATE: 2099-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN UNEY: 2.0
SOFTWARE: PATENTIN VET: 2.0
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Rana pipiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QDWLIFQKKGLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
OTHER INFORMATION: ribonuclease with Met at position 1 and Met24Leu
OTHER INFORMATION: substitution (recombinant Met(-1) RapERI Met23Leu)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                      98.4%; Score 570; DB 10; Length 105; 99.0%; Pred. No. 1.6e-58; ive 0; Mismatches 1; Indels (
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APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The Expressive of the States of America
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REPERENCE: 015280-34110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: WG PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ 1D NOS: 43
SOSTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 9, Application US/09948391A; Publication No. US20030027311A1
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                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFIWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.0
Matches 103; Conservative
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Best Local Similarity
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                                                                                                                   LENGTH: 105
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant OTHER INFORMATION: Met(-1) RaPLR1)
OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
                                                                                                                                   Length 105;
                                                                                                                                Score 569; DB 10;
Pred. No. 2.1e-58;
                                                                                                                                98.3%;
98.1%;
                                                                                                                                Query Match
Best Local Similarity
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FEATURE:

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| Sequence 28 | Application US/09961400 |
| Sequence 28 | Application US/09961400 |
| Sequence 28 | Application US/09961400 |
| Publication No. US20030124131A1 |
| GENERAL INFORMATION: |
| APPLICANT: RYBAK SUSANNA M. |
| APPLICANT: GOLDENBERG, DAVID M. |
| APPLICANT: NEWTON: CELLS |
| TITLE OF INVENTION: CELLS |
| TITLE OF INVENTION: CELLS |
| FILE REFERENCE: 018733/1059 |
| CURRENT APPLICATION NUMBER: US/09/961,400 |
| CURRENT PILING DATE: 2001-09-25 |
| PRIOR FILING DATE: 2000-08-17 |
| PRIOR FILING DATE: 1999-03-26 |
| PRIOR PILING DATE: 199
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                                                                                                                                                                                                          Rana pipiens ribonuclease (RaPLR1) Clone 5alb cDNA insert
                                                                                                                                                                                                                                                                                                                                                          Length 127;
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Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
                                                                                                                                                                                                                                                                                                                                                          Score 569; DB 10;
Pred. No. 2.7e-58;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 569; DB 10;
Pred. No. 2.7e-58;
1; Mismatches 1;
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Best Local Similarity 98.1%;
Matches 102; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 127
                                                                                                                                                                                                                                                                                                                                                      Query Match 98.3
Best Local Similarity 98.1
Matches 102; Conservative
                                              LENGTH: 127
TYPE: PRT
ORGANISM: Rana pipiens
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US-09-961-400-28
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OTHER INFORMATION:
US-09-948-391A-28
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US-09-948-391A-11
                   SEQ ID NO 28
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APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

TAPLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: UMMBER: US/09/961,400

CURRENT FILING DATE: 2001-09-25

PRIOR PELLING DATE: 2000-08-17

PRIOR FILING DATE: 1999-03-26

PRIOR PILING DATE: 1999-03-26

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR PILING DATE: 1998-03-26

NUMBER OF SEQ ID NOS: 43

COFTWARE PARENTED NOS: 43
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                                                                             QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
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               Gaps
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               1; Indels
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Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne I.
APPLICANT: Newton, Dianne I.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the APPLICANT: as represented by The Secretary of the APPLICANT: Department of Health and Human Services
TILE OF INVENTION: Recombinant Anti-Tumor RNase;
FILE REFERENCE: 015280-3431100S
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR APPLICATION NUMBER: US 08/622,613
PRIOR APPLICATION NUMBER: US 08/622,613
PRIOR FILING DATE: 1998-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 569; DB 10;
Pred. No. 2.1e-58;
1; Mismatches 1;
       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
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Best Local Similarity 98.1%;
Matches 102; Conservative
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Rana pipiens
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Matches 102;
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US-09-948-391A-13
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WS-09-961-400-11

Sequence 11, Application US/09961400

Publication No. US20030124131A1

GENERAL INPORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

TITLE OF INVENTION: CELLS

FILE REPERENCE: 018733/1059

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT FILING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: 09/622,613

PRIOR APPLICATION NUMBER: 09/622,613

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR PILING DATE: 1999-03-26

PRIOR PILING DATE: 1999-03-26

PRIOR SPLING DATE: 1999-03-26

PRIOR SPLING DATE: 1999-03-26

PRIOR SPLING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATCHIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.4%; Score 564; DB 10; Length 104; 98.1%; Pred. No. 8e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFFWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.1:
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-948-391A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-961-400-11
                                                                                                                                                                                                                                                                                                               LENGTH: 104
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LENGTH: 104
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                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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Sequence 13, Application US/09961400

bublication No. US20030124131A1

publication No. US20030124131A1

publication No. US20030124131A1

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: NEWTON, DIANNE L.

TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: CELLS

FILE REPREBRUCE: 018733/1059

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT FILING DATE: 2000-09-25

PRIOR PLING DATE: 2000-08-17

PRIOR PLING DATE: 1999-03-26

PRIOR PLING DATE: 1999-03-26

PRIOR PLING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PALENTIN VEF. 2.1

SEQ ID NO 13

LENGTH: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 DWLIFQKKHLINIRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens OTHER INFORMATION: ribonuclease with Met at position 1 and Gln2Ser OTHER INFORMATION: substitution (recombinant Met(-1) RaPLR1 Q1S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                 APPLICANT: Nyderon, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Serpresented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR PILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SEQ ID NOS: 43
LENGTH: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 97.4%; Score 564; DB 10;
Best Local Similarity 98.1%; Pred. No. 8.1e-58;
Matches 101; Conservative 1; Mismatches 1;
Sequence 13, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Rana pipiens
US-09-961-400-13
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Query Match 97.4%; Score 564; DB 10; Length 105;
Best Local Similarity 98.1%; Pred. No. 8.1e-58;
Matches 101; Conservative 1; Mismatches 1; Indels 0; Gaps
                                                                                                 62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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Search completed: May 7, 2004, 21:51:56 Job time : 34.3695 secs

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Compugen Ltd.
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compue
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- protein search, using sw model OM protein

7, 2004, 21:38:36; Search time 9.43686 Seconds (without alignments) 1060.090 Million cell updates/sec May Run on:

US-09-961-400-4 Title: Perfect score:

579 1 QDWLTFQKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* 1 2 6 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	**			SUMMARIES	
Score M	atch	Query Match Length	DB	ΠD	Description
544	94.0	104	N	A39035	ribonuclease-relat
<b>~</b>	48.9		7	A27121	ribonuclease-relat
279.5	48.3		Н	JX0120	ribonuclease-relat
5.	٠	5 111	7	JX0085	pancreatic ribonuc
~	24.5		7	841111	
<u>س</u>	21.2	124	Н	NRUI	
20	20.7	_	П	A32474	
œ	20.4		Н	NRGPB	~
7	20.2		Н	NRCU	
G	20.0	124	-	NRWHK	· U
112.5	19.4		Н	A35932	
_	19.2		Н	NRKS	
0	19.0	125	٦	B43825	
_	19.0		Н	NRYY	pancreatic ribonuc
2	18.7		~1	I52489	ribonuclease 4 (EC
m	18.7		Н	NRBOB	pancreatic ribonuc
m	18.7		Н	NRCB	pancreatic ribonuc
<u>~</u>			Н	NRBO	pancreatic ribonuc
7	18.5		7	S08549	ribonuclease - dom
106	18.3		Н	NRHUAG	angiogenin precurs
0.5	18.1		Н	NRSH	
ın	18.1	124	Н	NRPRH	pancreatic ribonuc
0.5	18.1		-	NRHP	
0.5	18.1		7	S07141	U
Ŋ	18.0		Н	A43825	
0.4	18.0		Н	NRWB	H.
0.4	18.0	124	Н	NRGN	
~	17.8		H	NRGF	
03	17.8	124	-	NRPG	pancreatic ribonuc

pancreatic ribonuc	pancreatic-type ri	pancreatic ribonuc	eosinophil-associa	pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc				pancreatic ribonuc	eosinophil-associa	pancreatic ribonuc	pancreatic ribonuc		н
NRPQ	\$20066	NRHO	JC6159	NRGPA	NRDEO	NRCM	NRCMM	NRCMB	S08546	NRGT	JC6160	NRANE	JX0115	NRANT	NREKN
_	٠.	ч	~	Н	Н	ч	н	гH	~	Н	7	ч	7	Н	Н
٠.	"														
128	167	128	155	124	124	124	124	124	124	124	156	124	119	124	124
	17.8 167 2														
17.8		17.6	17.5	17.3	17.1	17.1	17.1	17.1	17.0	16.9	16.9	16.8	16.7	16.6	16.6

# ALIGNMENTS

RESULT 1 A39035 rihonuclease-related anti-tumor protein - northern leonard from (frammet)
C:Species: Rana pipiens (northern leopard frod)
C;Date: 31-Jul-1991 #sequence revision 31-Jul-1991 #text change 30-Jun-1993
C; Accession: A39035
R; Ardelt, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A; Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocy
A; Reference number: A39035; MUID: 91093131; PMID: 1985896
A; Accession: A39035
A;Status: preliminary
A; Molecule type: protein
A; Residues: 1-104 <ard></ard>
C; Superfamily: pancreatic ribonuclease

ens oocytes and earl

0; Gaps Length 104; Indels Score 544; DB 2; Le Pred. No. 1.4e-47; 4; Mismatches 3; Query Match
Best Local Similarity 93.3%;
Matches 97; Conservative

0

9 9 1 EDWLIFQKKHITNIRDVDCDNIMSINLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLIT 1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKALCKGLIASKNVLTT g ਨੇ

RESULT 2

Cibecies: Rana catesbeiana (bullfrog)
Cibecies: Rana catesbeiana (bullfrog)
Cibecies: Rana catesbeiana (bullfrog)
Cibete: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993
Cibete: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993
Cibete: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993
Cibecession: K:; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanagi Biochemistry 26, 2189-2194, 1987
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A;Reference number: A27121; MUID:87299649; PMID:3304421
A;Reference number: A27121
A;Rolecule type: protein
A;Residues: 1-111 < TIT>
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pancreatic ribonuclease

Gaps . 8 / Match 48.9%; Score 283; DB 2; Length 111; Local Similarity 47.7%; Pred. No. 2.2e-21; les 53; Conservative 17; Mismatches 33; Indels Query Match Best Local Si Matches 53;

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C;Accession: A00827
R;Beintema, J.J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1983
A;Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amn A;Reference number: A92957; MUID:87036770; PMID:6571219
A;Accession: A00827
                                                                                                                                         (Iguana iguana) pancreatic ribonuclease. PMID:8307028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Comment: The cuis is a rodent belonging to the same subfamily as the guinea pig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QDWLTFQKKHL-----TNTRDVDCNNIL---STNLFHCKDKNTFIYSRPEPVKAIC--K 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DDWSSFQNKHIDYPETSASNPNAYCDLAMQRRNLNPTKCKTRNTFVHASPSEIQQVCGSG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TNTRDVDCNNIL---STNLFHCKDKNTFIYSRPEPVKAIC--KGI 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKFÓRQHMDSDGHPDÍNÍN--YCNEMMVRRSMIQGRCKPVNÍFVHEPLÉAVQAVČSQKNV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angiogenin [validated] - bovine
MyAlternate names: angiogenesis factor
NyContains: ribonuclease (EC 3.1.27.-)
Cypecies: Bos primigenius tauuns (cattle)
Cypecies: Bos primigenius tauuns (cattle)
Cypecies: A33474; S02001; A30044; S48212
Expecssion. A33474; S02001; A30044; S48212
Biochemistry 28, 6110-6113, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 PCKNGOINCYOSHSSMRITDCRVISSSKYPNCSYRMIOAOKSIIVACEGIPSVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 04-Oct-1996
                        C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 IASKNVLTTFEFY----LSDCNVTSRP----CKYKLKKSTNTFCVTCEN--QAPVHF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTHYEDNIYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Superfamily: pancreatic ribonuclease
C, Keywords: glycoprotein, hydrobas; nucleic acid digestion, pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;66.94,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIIASKNVLTTFE-FYLSDC----NVTSRPCKYKLKKSTNTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                              Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;94/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                     24.5%; Score 142; DB 2; Lengtu ... 29.8%; Pred. No. 3.1e-07; ... **: matches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.2%; Score 123; DB 1; Length 12.
28.2%; Pred. No. 2.6e-05;
ive 21; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Title: Amino acid sequence of bovine angiogenin. A, Reference number: A32474; MUID:89375344; PMID:2775757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 1-124 <BEI>
A;Note: about one-third of the molecules lacked Ala-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - cuis
                                                   C; Accession: S41111
R; Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A; Title: The amino acid sequence of iguana
A; Reference number: S41111; MUID:94139745;
C;Species: Iguana iguana (common iguana)
                                                                                                                                                                                                                                                                                                                 C; Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pancreatic ribonuclease (EC 3.1.27.5)
N;Alternate names: RNase 1; RNase A
C;Species: Galea musteloides (cuis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 21.2
Best Local Similarity 28.2
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 29.8
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LTFQKKHL----
                                                                                                                                                                                                   A; Accession: S41111
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-119 <ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                        A; Residues:
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                                                                                                                                                                                                                                                                                                                                                  K.; Kawauchi, H.; Takayanagi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: JX0085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; (
J. Biochem. 106, 729-735, 1989
A;Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A;Reference number: JX0085; MUD:90130374; PMID:2613682
A;Molecule type: protein
A;Residues: 1-111 < NIT>
                                                                                                                                                                                                                                                                                                       Cipaces incorporate and the sequence revision in Sep-1999 #text_ciange locations of Accession: JXX0120
R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takay J. Biochem. 108, 139-143, 1990
A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs. A;Reference number: JXX0120; MUID:91035319; PMID:2229005
A;Reference number: JXX0120; MUID:91035319; PMID:2229005
A;Residues: 1-111 cype: protein
A;Residues: 1-111 ckAM>A;Residues: 1-111 ckAM>A;Residues: 1-111 ckAM>A;Residues: 1-111 ckAM>A;Residues: 1-111 ckAM>A;Residues: 1-111 ckAM>A;Residues: 1-211 ckAM>A;Residues: 1-211 ckAM>A;Residues: 1-211 ckAM>A;Residues: 1-211 ckAM>A;Residues: 1-211 ckAM>A;Residues: acid (Gln) #status experimental F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ribonuclease-related sialic acid-binding lectin - Japanese frog
C;Species: Rana japonica (Japanese frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C'Keywords: hydrolase; pyroglutamic acid
F://Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10,35,104,Active site: His, Lips, His #status predicted
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted
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                                                         57 VLTTFEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENOAPVHFVGVGHC 104
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                        VLTTFEFYLSDC --- NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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44.1%; Pred. No. 4.8e-21;
live 19; Mismatches 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Mismatches
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C;Superfamily: pancreatic ribonuclease
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Best Local Similarity
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Matches 47; Conserv
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pancreatic ribonuclease (EC 3.1.27.5) - minke whale
NyAlternate names: RNase 1; RNase A
C)Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C)Bacide: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C)Accession: A00818
R)Emmens, M.; Welling, G.W.; Beintema, J.J.
B)cohem. J. 157, 317-323, 1976
A)Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A)Reference number: A00818; MUID:76277855; PMID:962870
A)Recession: A00818; MUID:76277855; PMID:962870
C)Superfamily: pancreatic ribonuclease
C)Residues: 1-124 < EMM>
C)Superfamily: pancreatic ribonuclease
C)Reywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
C)Reywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F)12,41,119/Active site: His, Lya, His #status predicted
F)26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F)76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coypu and chinchilla pancreatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 LCKNGQTNCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
                                                                                                                                                                                                                                                                                                                     6 MKEQRQHMDPBGSSPSNSSNY-CNVMMIRRNNTQGRCKPVNTFVHESLADVQAVCFQKNVL
                                                                                                                                                                                                                                                                           4 LIFQKKHL-----TNIRDVDCNNIL---SINLFHCKDKNIFIYSRPEPVKAIC--KGII
                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 CKNGQTNCYQSYSRMRITDCRVTSSSKFPNCSYRMSQAQKSIIVACEGDPYVPVHF 120
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                                                                                                                                                                                                                                                                                                                                                                                                            53 ASKNVLTTFEFY----LSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF 98
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                                                    experimental
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A.Molecule type: protein
A.Residues: 1-128 <VAN>
C.Superfamily: pancreatic ribonuclease
C.Superfamily: pancreatic ribonuclease
C.Keywords: glycoprotein; hydrolase; mucleic acid digestion; pancreas
F.12,41,119/Active site: His, Lys, His #status predicted
F.26-64,40-95,58-110,65-72/Disulfide bonds: #status predicted
F.34/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                              Length 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.00011;
ches 37; Indels
                                                                                                                                                                                                                Indels
      F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34/Binding site: carbohydrate (Asn) (covalent) #status ey
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R, van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of
A;Reference number: A90612; MUID:77065676; PMID:999896
                                                                                                                                          20.4%; Score 118; DB 1; L/
25.9%; Pred. No. 8.6e-05;
tive 25; Mismatches 39;
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C,Species: Myocastor coypus (nutria, coypu)
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Best Local Similarity 28.2.
Thes 33; Conservative
                                                                                                                                       Query Match
Best Local Similarity 25.94
Matches 30; Conservative
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Best Local Similarity
Thes 32; Conserve
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NRCU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Contents: annotation; conformation by (1)H-NMR, residues 1-125
R;Lequin, O.; Albaret, C.; Sontems, F.; Spik, G.; Lallemand, J.Y.
Biochemistry 35, 8870-8880, 1996
A;Title: Solution structure of bovine angiogenin by (1)H nuclear magnetic resonance sh;Title: Solution structure of bovine angiogenin by (1)H nuclear magnetic resonance sh;Reference number: A5881; MUID:96280645; PMID:8688423
A;Contents: annotation; conformation by (1)H-NMR
R;Reisdorf, C.; Abergel, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, Bur. J. Biochem. 224, 811-822, 1994
A;Title: Proton resonance assignments and secondary structure of bovine angiogenin. A;Reference number: S48212; MUID:95010071; PMID:7925406
A;Contents: annotation; conformation by (1)H-NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Cavia porcellus (guinea pig)
C; Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C; Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C; Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
E; Acan den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, Bur. J. Biochem. 75, 91-100, 1977
A; Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structum A; Reference number: A91247; MUID:77185023; PMID:862624
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                                                                                                                                                                                                                                                                                                                                                    A.Experimental source: milk
R.Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
Submitted to the Brookhaven Protein Data Bank, January 1995
A.Reference number: A65065; PDB:1401
A.Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125
A.Contents: annotation; R.; Riordan, J.F.; Vallee, B.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 2349-2953, 1995
A;Title: Crystal structure of bovine angiogenin at 1.5 Angstroms resolution.
A;Reference number: A58315; MUID:95224057; PMID:7708754
A;Contents: annotation; X-ray crystallography, 1.5 angstroms
R;Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
Submitted to the Brookhaven Protein Data Bank, April 1996
A;Reference number: A65709; PDB:1GIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 DEYCFNAMKONRRITRPCKDRNTFIHGNKNDIKAICEDRNGQPYRGDLRISKS-----EFQ
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    guinea pig (tentative sequence)

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                                                                                                                                C.; Montreuil, J.; Spik, G.; Tartar,
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A;Residues: 1-128 <VAN>
A;Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
                                                                                                                      R;Maes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar FEBS Lett. 241, 41-45, 1988
A;Title: The complete amino acid sequence of bovine milk angiogenin. A;Reference number: S02001; MUD:89065101; PMID:3197838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 120; DB 1; ]; Pred. No. 5.3e-05; 14; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 LSDC---NVTSR-PCKYKLKKSTNTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVDCNNILSTNLF--HCKDKNTFIYSRPEPVKAICK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreatic ribonuclease (EC 3.1.27.5) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.7%;
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                                                                                      A; Experimental source: plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: RNase IB
                        A; Molecule type: protein A; Residues: 1-125 < BON>
                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 1-125 < MAE>
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Best.Local Similarity
Matches 32; Conserv
A; Accession: A32474
                                                                                                                                                                                                                                                             A; Accession: S02001
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R.Bond, M.D.; Strydow, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A,Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernme
A,Reference number: S29833; MUID:93192291; PMID:8448182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Hydrochaeris hydrochaeris (capybara, carpincho)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 29-Oct-1999
C;Accession: A00824
B;Beintema, J.J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1983
A;Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amaly. Reference number: A92957; MUID:87036770; PMID:6571219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>ب</u>
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                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 CKDTNTFVHGNKGSIKDVCEDKNGKPYGKNFRISKSSFQVTTCKHVGGSPWPPCRYRAIS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LIFQKKHL-----INTRDVDCNNILSTNLF---HCKDKNTFIYSRPEPVKAIC--KGIIA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
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                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S29833; B43825
                                                                                                                                                                                                                                    64 PCKNGQSNCYESTSNMHITDCRLTSNSKFPDCLYRTSQEEKSIIVACEGNPYVVHF 120
                                                                                                                           98
                                                                                    FQKKHL-----TNTRDVDCNNIL-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: pyroglutamic acid
F;l/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 SKNVLTTEEFY----LSDCNVTSR----PCKYKLKKSTNTFCVTCENQ--APVHF 98
                                                                                                                                                                                                      58 -----LTTFEFYLSDCNVTSR----PCKYKLKKSTNTFCVTCENQ--APVHF
                              28;
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A;Molecule type: protein
A;Molecule type: protein
A;Notes: 1-125 <BON>
A;Note: submitted to the Protein Sequence Database, December 1992
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 128;
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A,Ablacule type: protein
A,Roblacule type: protein
C,Superfamily: pancreatic ribonuclease
C,Keywords: hydrolase; nucleic acid digestion; pancreas
C,Keywords: hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Indels
                              Indels
0.00043;
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;; Pred. No. 0.00053;
13; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pancreatic ribonuclease (EC 3.1.27.5) - capybara N,Alternate names: RNase 1; RNase A
C;Species: Hydrochaeris hydrochaeris (capybara, c
   28.2%; Pred. No. 0.00
ive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.0%;
29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 STNTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
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      Similarity
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Matches
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A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Coss-references: GB:U22516; NID:g726325; PIDN:AA491366.1; PID:g726326
C;Genetics:
A;Cross-references: GB:U22516; NID:g726325; PIDN:AA491366.1; PID:g726326
C;Genetics:
A;Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pancreatic ribonuclease nucleic acid degradation; pyroglutamic acid
E;1-24/Domain: signal sequence #status predicted <NAT>
F;25-145/Product: angiogenesis; hydrolase; nucleic acid (GIN)
F;25-Modified site: pyrrolidone carboxylic acid (GIN)
F;25/Modified site: pyrrolidone carboxylic acid (GIN)
F;37,64,137/Active site: His, Lys, His #status predicted
F;50-104,63-115;81-130/Disulfide bonds: #status predicted
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R. Beintema, J.J.; Knol, G.; Martena, B.
B. Brichim. Biophys. Acta 705, 102-110, 1982
A. Title: The primary structures of pancreatic ribonucleases from African porcupine and A. Reference number: A90644; MUID:83000399; PMID:7115727
A. Accession: A00821
A. Molecule type: protein
A. Molecule type: protein
A. Residues: 1-128 < BEI>
C.; Superfamily: pancreatic ribonuclease
C.; Reywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
C.; Reywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
C.; Reywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F: 26-110, 65-72 Disulfide bonds: #status predicted
F: 36-10, 65-72 Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                    62 NVLCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120
                                 LTPQKKHLTNTRDVD-----CNNILSTNLF---HCKDKNTFIYSRPEPVKALCKGIIASK 55
                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                        N.Alternate Fames: angiogenesis factor
N.Concains: ribonuclease (EC 3.1.27.-)
C.Species: Mus musculus (house mouse)
C.Species: Mous musculus (house mouse)
C.Accession: A35932
R.Bond, M.D.; Vallee, B.L.
R.Bond, M.D.; Vallee, B.L.
A;Title: Isolation and sequencing of mouse angiogenin DNA.
A;Reference number: A35932; MUID:91025023; PMID:2222458
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C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 30-Sep-1993
                                                                  30 CKDKNTFIYSRPEPVKAIC--KGIIASKNV-LTTFEFYLSDCNVTS----RPCKYKLKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.4%; Score 112.5; DB 1; 34.2%; Pred. No. 0.00034; tive 11; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pancreatic ribonuclease (EC 3.1.27.5) - casiragua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 111;
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Best Local Similarity
Matches 26; Conserv
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à q ð g us-09-961-400-4.rpr

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66 KNGQTNCYQSYSSMHITDCRVTSNSKFPDCSYRTTQAQKSIVVACEGNLYVPVHF 120
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A/Status: preliminary
A/Molecule type: DNA
A/Residues: 29-53, D', 55-147 <ROS>
A/Residues: 29-53, D', 55-147 <ROS>
A/Residues: 29-53, D', 55-147 <ROS>
B/S. Chous, Teferences: EMBL:U36775; NID:g1040977; PIDN:AAA96750.1; PID:g1040978
B/S. Zhou, H.M., Strydom, D.J.
Bur. J. Biochem. 217, 401-410, 1993
A/Title: The amino acid sequence of human ribonuclease 4, a highly conserved ribonucleas
A/Reference number: S38272; MUID:94039064; PMID:8223579
                                                                                                                                                                                                                                                                                                                                                                                              A.Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-147 <RES.
A,Residues: 1-147 <RES.
B,Resemberg, H.F.; Dyer, K.D.
Nucleic Acids Res. 23, 4290-4295, 1995
A,Title: Human ribonuclease 4 (RNase 4): coding sequence, chromosomal localization and A,Recession: S60163; MUID:96091174; PMID:7501448
RESULT 15
152489
Tibonuclease 4 (EC 3.1.-.-) precursor - human
N;Alternate names: RNase 4
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
C;Date: 02-Jul-1996 #sequence_revision (f. Kosaka, M.; Tada, H.; Yamada, H. Biochim. Biophys. Acta 1261, 424-426, 1995
Bjochim. Biophys. Acta 1261, 424-426, 1995
A;Attle: Molecular cloning and expression of human ribonuclease 4 cDNA.
A;Reference number: 152489; MUID:95260866; PMID:7742370
A;Accession: 152489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.7%; Score 108.5; DB 2; Length 147; 31.2%; Pred. No. 0.00088; Live 16; Mismatches 44; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Gener: GDB:RNASE4
A.Cross-references: GDB:6108046; OMIM:601030
A.Map position: 14q24-q31
A.Introns: #status absent
C.Superfamily: pancreatic ribonuclease
C.Keywords: hydrolase
F:40,68,144/Active site: His, Lys, His #status predicted
F:53-109,67-120,85-135,92-99/Disulfide bonds: #status predicted
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Best Local Similarity 31.24
Matches 35; Conservative
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Search completed: May 7, 2004, 21:54:53 Job time: 9.43686 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 7, 2004, 21:30:40 ; Search time 5.25351 Seconds (without alignments) 1030.796 Million cell updates/sec Run on:

US-09-961-400-4 579 1 QDMLTFQKKHLTNTRDVDCN....TFCVTCENQAPVHFVGVGHC 104 Title: Perfect score: Sequence:

Scoring table:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description		P22069 rana pipien	5 rana	rana	P14626 rana catesb	7 iquan	m		P00680 galea muste		6	P00676 myocastor c	~		_	Q8wn64 papio hamad		Q8hzq0 pan troglod		P31347 oryctolagus	_		P34096 homo sapien		P00656 bos taurus	O35290 mus musculu	homo	8 pan t	P07847 aepyceros m	P00668 antilocapra	P00672 hippopotamu	51	P31346 sus scrofa	29 saimiri s
COLLABORATION	ID	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RN30 RANPI	RNPO RANCA	LECS_RANJA	RNPL RANCA	RNP IGUIG	ANGE MOUSE	ANGI CERAE	RNP GALMU	ANGI BOVIN	RNPB_CAVPO	RNP MYOCO	RNP_BALAC	ANGI MACMU		ANGI_PAPHA		RNS4 PANTR	ECP4_MOUSE	ANGI_RABIT	RNP HYDHY	ANGI_MIOTA	RNS4_HUMAN	RNP_CHIBR	RNP_BOVIN	ECP3_MOUSE		ANGI_PANTR		RNP ANTAM	RNP_HIPAM		ANGI PIG	
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## ALIGNMENTS

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Glycobiology 3:37-45(1993).
                                                                [5]
STRUCTURE BY NMR OF 23-133.
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Best Local Similarity
                                                catesbeiana eggs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 AA;
CHARACTERIZATION.
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01-0CT-1989 (Rel. 12, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Ribonuclease, occytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
                                                                                                                                                                                                              1 ODWLTPOKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIŜSUE=EGG;
MEDLINE=87299649; PubMed=3304421;
Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
Takayanagi G., Hakomori S.;
"Amino acid sequence of sialic acid binding lectin from frog (Rana
                                                                                                                                                                                                                                                                                                                                                                                                                       Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
"The Rana catesbelana rcr gene encoding a cytotoxic ribonuclease.
Tissue distribution, cloning, purification, cytotoxicity, and active
residues for Rases activity.";
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";
Nucleic Acids Res. 20:1371-1377(1992).
                                                                                                                                                                Length 104;
                                                                                                                                                                                                                                FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                               61 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                Indels
                                                                                                                                                 11845 MW; 22A753C2F9E566B4 CRC64;
                                                                                                                                                                94.5%; Score 547; DB 1; L. 94.2%; Pred. No. 5.5e-52; ive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                         133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION, AND SEQUENCE OF 81-101.
MEDLINE=92220613; PubMed=1373237;

    Biol. Chem. 273:6395-6401(1998).

                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Liver;
MEDLINE=98165825; PubMed=9497370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 26:2189-2194(1987).
                                                                                                                                                                                                                                                                                                                                                         Rana catesbeiana (Bull frog).
                                                                                                                                                                        Local Similarity 94.2
es 98; Conservative
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                                                                                                                                                 104 AA;
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MAILLE K., Oyana F., Oyana K., Sekgachi K., Kawauchi H.,

MAILLE K., Oyana F., Oyana K., Sekgachi K., Kawauchi H.,

MAILLE K., Oyana F., Oyana K., Sekgachi K., Kawauchi H.,

MAILLE K., Oyana F., Oyana K., Sekgachi K., Kawauchi H.,

MAILLE S., Oyana P., Salica C., Titani K.,

MAILLE B., MAILLE S., MAILLE B., MAILL
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QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
                          1 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Egg;
MEDLINE=91035319; PubMed=2229005;
Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
Takayanagi Y., Titani K.;
Takayanagi Y., Titani K.;
                                                                                                                                                                                                                                                                                                                                                                                                                          Rana japonica (Japanese reddish frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                              82 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLTTFEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
Probom; PR000535; RNaseA; 1.
SMART; SM00092; RNASE Pc; 1.
PROSITE; PS00127; RNASE PANCRATIC; 1.
Hydrolase; Nuclease; Endomuclease; Sialic acid; Lectin; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12326 MW; FDEBDDF3834ED679 CRC64;
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Pred. No. 2.9e-23;
9; Mismatches 36
                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (Rel. 16, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sialic acid-binding lectin (EC 3.1.27.-)
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RNPL RANCA
ID RNPL RANCA
AC P14626;
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P18839;
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                                                                                                                                     TISSUE=Liver;
MEDLINE=90130374; PubMed=2613682;
Nitte R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
Nitte R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
Nataki T., Ohgi K., Irie M.;
"Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eŭkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
NCBI_TaxID=8517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ELSTISFKINICIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 VLTTFEFYLSDC---NVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphooligonucleotides ending in C-P or with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family. PIR, JX0088; JX0085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The amino acid sequence of iguana (Iguana iguana) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P80287;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
                                                                                                                                                                                                                                                                                                                                    38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D64BA72456C10788 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.5e-21;
01-APR-1990 (Rel. 14, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
RB-FBB-2003 (Rel. 41, Last annotation update)
RB-Danoclease, liver (BC 3.1.27.5).
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.5%; Score 263.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao W., Beintema J.J., Hofsteenge J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ribonuclease.";
Eur. J. Biochem. 219:641-646(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Pancreas;
MEDLINE=94139745; PubMed=8307028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12461 MW;
                                                                                                                                                                                                                       J. Biochem. 106:729-735(1989)
                                                                                                                                                                                                                                                                                                                                InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                   1 QDWLTFQKKHL-----TNTRDVDCNNIL---STNLFHCKDKNTFIYSRPEPVKAIC--K 49
                                                                                                                                                                                                                                                                                                                                                                                                                                09
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 ODWSSFONKHIDYPETSASNPNAYCDLMMQRRNLNPTKCKTRNTFVHASPSEIQQVCGSG
                                                                                                                                                                                                                                                                                                                                                                          16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2',3'-cyclic phosphate intermediates.
-!- SUBCELULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 GIIASKNVLTTFE-FYLSDC----NVTSRPCKYKLKKSTNTFCVTCENQAPVHF
                                                                                                                                                                                                 Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
MOD_RES
1 1 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                           Length 119;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                            BY SIMILARITY.
W, 6072PBSB7B15BD5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                       45;
                                                                                                                                                                                                                                                                                                                                            24.5%; Score 142; DB 1; 29.8%; Pred. No. 1.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       19; Mismatches
                                                                                                                                        PRINTS, PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe_PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angiogenin-related protein precursor ANGRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=129; IISSUE=Liver;
MEDLINE=96079109; Pubmed=8530072;
                                                                                                                                                                                                                                                                                                   113 B
13324 MW;
                                                                                                   HSSP; P00656; 1LSQ.
InterPro; IPR001427; RNaseA.
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InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U22519; AAA91367.1; -. HSSP; P03950; 1A4Y.
                                                                                                                             Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                80
91
                                                                                  PIR; S41111; S41111.
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                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       34;
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MOUSE
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Pfam; PF00074; rnaseA; 1.

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"niversifying selection of the tumor-growth promoter angiogenin in primate evolution.";

Mol. Biol. 19:438-445(2002).

--- FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity).

--- SUMCELIULAR LOCATION: Secreted.

--- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                             ---PCKYKLKKS
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                 21.5%; Score 124.5; DB 1; Length 145; 36.8%; Pred. No. 1.7e-06; cive 11; Mismatches 30; Indels 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anglogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                                                                                                                                           ANGIOGENIN-RELATED PROTEIN.
PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                           30 CKDKNTFIYSRPEPVKAIC--KGIIASKNV-LTTFEFYLSDCNVTSR-
                                                                                                                                                                                                                                                                                                              29A6EB814429C4AD CRC64;
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es 30;
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ProDom; PD000555; RNaseA; 1.
SWART; SW00092; RNAse Pc; 1.
PROSTE; PS00127; RNASE PROCREATIC; 1.
Signal; Hydrolase; Nuclease; Endonuclease;
Signal, Agrolase; Nuclease;
Signal, Agrolase; Indonuclease;
Signal, Agrolase; Indonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
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MEDLINE=21918422; PubMed=11919285;
                                                                                                                                                                                                                                                                                         130 BY
16612 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seg
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InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 FRYIIIGCENGWPVHF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 INTFCVTCENQAPVHF 98
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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25
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137
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145 AA;
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119
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  ACT SITE
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Matches
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                                                                                                                                                                                                         5 TFQKKHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAIC---KGIIASKNV-LTT 60
                                                                                                                                                                                                                         53 TMRRRHLTSP-------CKDINTFIHGNRHHIKAICGDENGNPYGENIRISK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                              Beintema J.J., Newtebboom B.;

"Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amino acid sequences with those of two close relatives:
capybara and cuis ribonuclease.";
J. Mol. Evol. 19:145-152(1983).
-! GATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphacoligonucleotides ending in C-P or U-P
with 2', 3'-cyolic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                              Galea musteloides (Cuis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Hystricognathi, Caviidae, Galea.
                               Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
SIGNAL 1 24 BY SIMILARITY.
CHAIN 25 146 ANGIOGENIN.
                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                      21.5%; Score 124.5; DB 1; Length 146;
                                                                          PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
                                                                                                                                                                                        31; Indels
                                                                                                                                                                                                                                                          27860112E85B8DF9 CRC64;
                                                                                                                                                                                                                                               61 FEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVH 97
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                SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PANCREATIC; 1.
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InterPro; IPR01427; RNaseA.
InterPro; IPR001427; RNaseA.
Pfam, PF000794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; I.
SMART; SM00902; RNASE PA.
HYGROLIES; PS00127; RNASE PANCREATIC;
HYGROLIASE; Nuclease; Endonuclease.
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87036770; PubMed=6571219;
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PRINTS; PR00794; RIBONUCLEASE.
                                                                                                                                                  16444 MW;
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          PD000535; RNaseA; 1
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                STANDARD;
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4 LTFQKKHL-----TNTRDVDCNNIL---STNLFHCKDKNTFIYSRPEPVKAIC--KGI 51
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                                                                                                                                                                                                                                                                                                                                              6 MKFOROHMDSDGHPDTNTN--YCNEMNVRRSMTQGRCKPVNTFVHEPLEAVQAVCSQKNV
                                                                                                                                                                                                                                                                                                                                                                                                                 52 IASKNVLTTFEFY----LSDCNVTSRP----CKYKLKKSTNTFCVTCEN--QAPVHF 98
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Biochemistry 35:8870-8880(1996).
-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
                                                                                                                                                                                                              24; Gaps
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BOS taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maes P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A.; "The complete amino acid sequence of bovine milk angiogenin."; FEBS Lett. 241:41-45(1988).
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Lequin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
"Solution structure of bovine angiogenin by 1H nuclear magnetic
                             1 1 MISSING (IN 1/3 OF THE MOLECULES)
124 AA; 13870 MW; 609C7E251A7BBA25 CRC64;
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"Crystal structure of bovine angiogenin at 1.5-A resolution.";
Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning, sequencing, and expression of bovine angiogenin."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                        DB 1; Length 124;
                                                                                                                             ch 21.2%; Score 123; DB 1; Length 12.
1 Similarity 28.2%; Pred. No. 2e-06;
33; Conservative 21; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANGI BOVIN STANDARD; PRT; 148 AA. P10152; O9GRP9; 10, Created) 20-MAR-1989 (Rel. 10, Created) 21-MAR-2004 (Rel. 41, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Angiogenin-1 precursor (EC 3.1.27.-).
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"Amino acid sequence of bovine angiogenin.";
BY SIMILARITY.
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Myocastor coypus (Coypu) (Nutria)
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21-JUL-1986 (Rel. 01, Last seqn
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                               InterPro; IPR001427; RNaseA.
PFfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
PRODOM; PD000535; RNASEA; 1.
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HSSP; P00656; 1SRN.
InterPro; IPR001427; RNaseA.
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25.9%;
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95
110
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12
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                                                                                                                                             PIR; A00826; NRGPB
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12
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Best Local
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                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs. Binds tightly to placental ribonuclease inhibitor and has very low ribonuclease activity. SubcELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Server and milk.
SIMILARITY: Belongs to the pancreatic ribonuclease family.
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MEDILNE-77185023; PubMed=862624;
Van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastra W.,
Beintema J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary structure and glycosidation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).
Cavia porcellus (Guinea pig).
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Protein synthesis inhibitor, Signal, 3D-structure.
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Pred. No. 5.2e-06;
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PROSITE; PS00127; RNASE PANCREATIC; 1.
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ProDom; PD000535; RNaseA; 1.
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InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
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P00679;
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-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2', 3'-cyclic phosphate intermediates.
-!- SUBCELIULAR LOCATION: Secreted.
-!- INSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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Eur. J. Biochem. 75:91-100(1977).
-!-CATANTUR CATTUTTY: Endonucleotide sending in C-P or U-P phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
-!-SUBCEILULAR LOCATION: Secreted.
-!- SUBCEILULAR LOCATION: Pancreas.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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Mammalia, Eutheria, Rodentia, Hystricognathi, Myocastoridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 128;
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28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A2F4101A1A33E93B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Nuclease; Endonuclease; Glycoprotein. DISULFID 26 84 BY SIMILARITY. DISULFID 40 95 BY SIMILARITY.
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N-LINKED (GLCNAC...
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Pred. No. 7.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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6 FQKKHL-----INTRDVDCNNIL-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LCKNGQINCYQSNSNMHIIDCRVISNSDYPNCSYRISQEEKSIVVAČEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 L------TTFEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3'-
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"The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
Bukaryota; Metazota; Chordeta; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Cetacea; Mysticeti;
Balaenopteridae; Balaenoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 117; DB 1; Length 128;
; Pred. No. 9.2e-06;
19; Mismatches 37; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Nuclease; Endonuclease; Glycoprotein.
DISULFID 26 84 BY SIMILARITY.
DISULFID 58 110 BY SIMILARITY.
ACT SITE 12 12 BY SIMILARITY.
ACT SITE 12 12 BY SIMILARITY.
ACT SITE 19 19 BY SIMILARITY.
ACT SITE 119 119 BY SIMILARITY.
ACT SITE 110 BY SIMILARITY.
ACT SIMILARI
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                               4EB924E52B445832 CRC64;
                                    ProDom; PD000535, RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSTITS, PS00127; RNASE Pc; 1.
Hydrolase; Nuclease; Endonuclease; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC
                                                                                                                                                                              BY SIMILARITY.
N-LINKED (GLCNA.
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PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=76277855; PubMed=962870;
                                                                                                                                                                                                                                                                                                                                                                                     119 BY
34 N-
14267 MW;
   PRINTS; PR00794; RIBONUCLEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00074, rnaseA; 1.
PRINTS; PR00794, RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
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InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Conservative
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110
72
12
41
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P00673;
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AC PNAP BALAC
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                                                                       4 LIFOKKHLINIRDVD-----CNNILSINLF---HCKDKNTFIYSRPEPVKAICKGIIASK 55
                                                                                                6 MKPQRQHMDSGNSPGNNPNYCNQAMMRRRWTQGRCKPVNTFVHESLEDVKAVC----SQK 61
                                                                                                                                                                62 NVLCKNGRINCYESNSTMHITDCRQTGSSKYPNCAXKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                              --TIFEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primate evolution...;
Mol. Biol. Bvol. 19:438-445(2002).
-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
to actin on the surface of endothelial cells; once bound,
angiogenin is endocytosed and translocated to the nucleus, thereby
promoting the endothelial invasiveness necessary for blood vessel
formation. Angiogenin induces vascularization of normal and
malignant tissues. Abolishes protein synthesis by specifically
hydrolyzing cellular tRNAs (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=21918422; PubMed=11919285;
Zhang J., Rosenberg H.F.;
"Diversifying selection of the tumor-growth promoter angiogenin in
                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00127; RUMGE PANCREATIC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
HydroLase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
                                             28;
                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            !- SIMILARITY: Belongs to the pancreatic ribonuclease family.
     20.0%; Score 116; DB 1; Length 124; 26.9%; Pred. No. 1.1e-05; ive 16; Mismatches 43; Indels ;
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                                                                                                                                                                                                                                                                        146 AA
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BY SIMILARITY.
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28-FEB-2003 (Rel. 41, Last segn
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PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
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InterPro; IPR001427; RNaseA.
                                      Conservative
                                                                                                                                                                                                                                                                    STANDARD;
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                     Similarity
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64
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Query Match
Best Local Simi
Matches 32;
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83 TNTFCVTCENQAPVHF
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115
130
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137
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145 AA;
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KETAINE-EVB/N; TISSUE-Liver;

KETAINE-EVB/N; TISSUE-Liver;

KETAINE-E2388257; PubMed=12477932;

KETAINE-EVB/N; TISSUE-Liver;

KARINESEZSER, L., Feingold E.A., Garue L.H., Derge J.G.,

KIAUSHER R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Kichards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Khiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

Rotherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Reneration and initial analysis of more than 15,000 full-length

Human and mouse colMa sequences "I."
                                                                                           09
                                                                                                                            -----CKDINTFVHGNRHHITAICGDENGSPYGGNLRIST 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regions.",
Biochim. Biophys. Acta 1162:177-186(1993).
Biochim. Biophys. Acta 1162:177-186(1993).

-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
-!- cactin on the surface of endothelial cells; once bound,
angiogenin is endocytosed and translocated to the nucleus, thereby
promoting the endothelial invasiveness necessary for blood vessel
formation. Angiogenin induces vascularization of normal and
malignant tissues. Abolishes protein synthesis by specifically
hydrolyzing cellular tRNAs.
                                                                                         5 TFQKKHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAIC---KGIIASKNV-LTT
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97192291; PubMed=8448182;
Bond M.D., Strydom D.G., Vallee B.L.,
"Characterization and sequencing of rabbit, pig and mouse
anglogenins: discernment of functionally important residues and
                                                     23;
                                                                                                                                                                                                                                                                                                                                                01-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                     DB 1; Length 146;
                                                         Indels
                                                                                                                                                                                         98 SPFQVTTCKLRGGSPRPPCQYRATRGSRNIVVGCENGLPVH 138
                                                                                                                                                                  61 FEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVH 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=91025023; PubMed=2222458;
Bond M.D., Vallee B.L.;
"Isolation and sequencing of mouse angiogenin DNA.";
Biochem. Biophys. Res. Commun. 171:988-995(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                         33;
                     19.9%; Score 115.5; DB 1
27.7%; Pred. No. 1.5e-05;
:ive 17; Mismatches 33
                                                                                                                                                                                                                                                                                                                                    01-MAY-1991 (Rel. 18, Created)
                                                           28; Conservative
                                                                                                                                                                                                                                                                                              STANDARD;
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53 TMRRRHLTSP-
                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                              ANGI MOUSE P21570;
                                                                                                                                                                                                                                                                               MOUSE
                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 CKDKNTFIYSRPEPVKAIC--KGIIASKNV-LTTFEFYLSDCNVTS----RPCKYKLKKS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Zhang J., Rosenberg H.F.;
"Diversifying selection of the tumor-growth promoter angiogenin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Papio hamadryas (Hamadryas baboon).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase, Nuclease, Endonuclease, Angiogenesis,
Protein synthesis inhibitor, Signal, Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
ANG OR RNASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANGIOGENIN.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06944260BB764938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SMO092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Ang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                  EMBL, BC055355; AAH55355.1; -. PIR, A35932; A35932.
HSSP, P03950; 1A4Y.
MGD, MGI-88022; Ang.
InterPro, IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16228 MW;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tENRAs (By similarity).

SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                   EMBL; AP441666; AAL61648.1; -
InterPro; IPR001427; RNaseA.
Prem; PP00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
PRODOW; PD000535; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
SIGNAL 1 24 BY SIMILARITY.
CHAIN 25 146 ANGIOGENIN.
                                                                                                                                                                                                                                                                                                                                                                                      ANGLOSOLIDONE CARBOXXLIC ACID (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A4C3CED1482370FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY.

SIMILARITY.

SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16432 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 27.79
                                                                                                                                                                                                                                                                                                                                                               24
146
25
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64
138
105
116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     64
138
50
63
63
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ACT_SITE
DISULFID
DISULFID
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ACT_SITE
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MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Search completed: May 7, 2004, 21:53:03 Job time : 5.25351 secs

SPRQVITCKLHGGSPRPPCRYRAIRGSRNIVVGCENGLPVH 138 61 FEFYLSDCNV----TSRPCKYKLKKSTNTFCVTCENQAPVH 97

TFOKKHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAIC---KGIIASKNV-LTT 60 | :::|||: 53 TMRRRHLTSP------CKDINIFIHGNRHHINAICGDENGNPYGGNLRISK 97

ŏ đ  $\overset{\circ}{\circ}$ g

19.4%; Score 112.5; DB 1; Length 146; 27.7%; Pred. No. 3.2e-05; tive 16; Mismatches 34; Indels 23

Gaps

23;

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

using sw model protein search, OM protein

7, 2004, 21:25:55; Search time 44.7895 Seconds May Run on:

(without alignments)
662.376 Million cell updates/sec

US-09-961-400-6

Title: Perfect score:

583 1 MQDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A\_Geneseq\_29Jan04:\* 1: genesecn198^~geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2002s:\* geneseqp2003as:\*
geneseqp2003bs:\* geneseqp1980s:\* geneseqp1990s:\*

Pred. No. is the number of results predicted by chance to have a SCOre greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2004s:

SUMMARIES	ID Description	AAY28867 becombine	9 SACVER 6	AAV2RRF Pana	727 Z2002	Aav28879	Recon	0	4		, Q	Ω	Aaw35130	à			2		ρ	α	ρ	ρ	pr	<u>,</u>	Aar47303	
	DB	. 7		2				2	•		•		·			•		2		-			•	•		
	Length 1	105	105	104	105	127	104	104	104	105	105	355	358	104	104	104	112	251	254	355	355	366	379	104	104	
. 0/0	Query Match	100.0	99.5	99.1	1.66	99.1	98.6	98.3	95.7	95.7	95.7	95.7	95.7	95.4	95.4	95.4	95.4	95.4	95.4	95.4	95.4	95.4		4.		
	Score	583	580	578	578	578	575	573	558	558	558	558	558	256	256	556	556	556	556	556	226	256	556	553	553	-
	Result No.		7	ю	4	ស	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	

Aaw14065 Onconase Aaw06543 Antitumou Aaw88233 Rana pipi Aav31329 Fron onco			AM931617 Northern Am935127 R. pipien Am935131 R. pipien Am935120 R. pipien Am93510 R. pipien	R. Ran Fro
AAW14065 AAW06543 AAW88233 AAX33322	AAW35116 AAW35122 AAW35117 AAW30302	AAW35115 AAW18224 AAB31667	ABG3161/ AAW35127 AAW35131 AAW35120 AAW35128	AAW35121 AAW35119 AAW88234 AAY33321
0000	0000	4 4 4	00000	0000
101 101 401 404	105 106 107	105	358 358 107 360	111 83 83 111
0 0 0 0 4 4 0 0 0 0 0	94.5 94.5 0.4.5	94.0	93.8 93.8 90.6 9.6	82.9 76.3 76.3
553 553 553	551 551 551 550	550 548 548	5 2 4 4 7 7 8 8 8 9 5 8 8 8 9 5 8 9 5 8 9 5 9 5 9 9 5 9 9 9 9	483.5 445 445 289
26 27 28 29	9 9 9 9 9 7 7 8	4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	3 8 8 8 4 4 8 6 0 11	4 4 4 4 2 6 4 7

## ALIGNMENTS

RESULT 1 AAY28867

AAY28867 standard; protein; 105 AA.

AAY28867; 

(first entry) 25-JAN-2000

Recombinant Met(-1) RaPLR1

Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase; covalently bound; LL2 antibody; ligand binding molety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease.

Rana pipiens. Synthetic.

Location/Qualifiers Misc-difference

/note= "Met not found in wild type RaPLR1"

WO9950398-A2

07-0CT-1999.

99WO-US006641. 26-MAR-1999;

98US-0079751P. 27-MAR-1998; (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Newton DL; Rybak SM,

WPI; 1999-610847/52. N-PSDB; AAZ08126.

for New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.

Claim 34; Page 57; 71pp; English.

The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Met at position 1. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant

cancerous B cells or human chorionic gonadotrophin (hCG) effective

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ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in frame with ligand binding moieties to form cycotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "(His)6 histidine tag attached to N-terminal Met'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                               MODWLTFOKKHLTNTRDVDCNNIMSTNLFHCKDKNTF1YSRPEPVKAICKG11ASKNVLT
                                                                                                                                                                                                                        1 MQDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                                                                                                                                                                   Gaps
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                                                                                                                                     Length 105;
                                                                                                                                                                                                                                                                           61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                         TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Met not found in wild type RaPLR1"
                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
                                                                                                                                                                   0
                                                                                                                                     Score 583; DB 2;
Pred. No. 1.1e-62;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             AAY28869 standard; protein; 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; frog; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 59; 71pp; English
                                                                                                                                      100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                  105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-610847/52.
                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB: AAZ08127.
                                                                                                          Sequence 105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pipiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                   Matches
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AAY28869
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     against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moleties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                              09
                                                                                                                                                                                                                                                                              09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rana pipiens liver ribonuclease, RaPLR1; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog; human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                            1 MODWLIFQKKHLINIRDVDCNNILSINLFHCKDKNIFIYSRPEPVKAICKGIIASKNVLI
                                                                                                                                                                                                                                            1 MQDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                           ·;
                                                                                                                                                                       Length 105;
                                                                                                                                                                                                                                                                                                                                        TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                   61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                         Score 580; DB 2; Length 10.
Pred. No. 2.6e-62;
                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana pipiens liver ribonuclease (RaPLR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US006641.
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                                                                                                                                                                         99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY28865 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                            Local Similarity 99.0
es 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ08124
                                                                                                                                          Sequence 105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09950398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-1999;
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                                                                                                                                                                             Query Match
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                                                                                                                                                                                                               Matches
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Sequence 104 AA;

The present sequence is a recombinant Rana pipiens ribonuclease protein (RapEngl) with Met at position 1 attached to (His)6 tag and Met24Leu. Carboxy terminal end of recombinant RapEngl has a covalently bound binding moiety, which can be a LL2 antibody directed against CD22 on

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99.08;

Best Local Similarity

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                                                                         61
                                                                                         OPWLTFQKKHLTNTRDVDCNNINSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
                                                                                                                                                                                                                                                                                                                                             Recombinant Met (-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease; RNase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant ribonucleases, used for killing target cells, e.g. for uting cancers, viral infections or autoimmune diseases.
                                                                QDWLTFQKKGLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                            Gaps
                                           ò
             Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Met not found in wild type RaPLR1"
                                                                                                                         SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                             SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                       4.4e-62;
1es 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                                                                                                                 Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.
            DB 2;
99.1%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 34; Page 61; 71pp; English.
                                                                                                                                                                                                                              AAY28871 standard; protein; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US006641
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                                                                                                                                                                                                                                                                                         (first entry)
      Query Match
Best Local Similarity 100.
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Newton DL;
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Synthetic.
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                                                                                                                          62
                                                                                                                                                                                                                                                          AAY28871;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a Rana pipiens Clone 5alb ribonuclease (RaPLRI). It is encoded by Clone 5alb cDNA obtained from Rana pipiens liver mRNA library. It exhibits differences with Oncoase (RTM) at amino acid residues 11, 20, 85 and 103. Carboxy terminal end of RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerrous B cells or human chorionic conductorphin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytocoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                9
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                                                               MSDWLTEQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                                          1 MQDWLIFQKKHLINIRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKALCKGIIASKNVLT
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                 Gaps
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                 ; 0
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/label= Rana_pipiens_Clone_Salb_ribonuclease
                                                                                                                           TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                     TSEFYLSDCNVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 105
                 Indels
Pred. No. 4.5e-62;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .23
/label= Signal_peptide
/note= "Putative"
24. .127
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                                                                                                                                                                                                                                                                                                         Rana pipiens Clone 5a1b ribonuclease
                                                                                                                                                                                                                AAY28879 standard; protein; 127 AA
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                                                                                                                                                                                                                                                                            (first entry)
              104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Rana pipiens,
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                                                                                                                                                                                                                                             AAY28879;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                AAY28879
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Sequence 105 AA;

autoimmune diseases

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covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadorrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytocoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                Recombinant Rana pipiens ribonuclease; RaPLR1 Gln1Ser; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; frog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Gln1Ser. Carboxy terminal end of recombinant RaPLR1 has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
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                                                                                                                           61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild type Gln replaced with Ser"
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                                                                                                                                                                                                                                                                                                                                                                     Recombinant RaPLR1 Gln1Ser amino acid sequence.
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Matches 103; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Misc-difference
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Synthetic.
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diseases
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                                                                                        61
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                                                                                    2 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKALCKGIIASKNVLTT
                                                                                                                              24 ODWLIFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEFVKAICKGIIASKNVLTT
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                                                  Gaps
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Pred. No. 1e-61;
1; Mismatches 0; Indels
        Length 127;
                                                                                                                                                                                             SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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                                                Indels
                             .7e-62;
s 0;
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99.1%; Sco. 100.0%; Pred. No. ... 0; Mismatches
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Best Local Similarity 99.0
Matches 103; Conservative
        Query Match
Best Local Similarity 100.
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disease.
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Rana pipiens. Synthetic.

25-JAN-2000

AAY28866;

AAY28866

62

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26-MAR-1999; 27-MAR-1998;

07-OCT-1999

WO9950398-A2

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Gaps

0

Length 104; Indels

proteins. diseases

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AAW35115 to AAW35123 encode recombinant proteins (ronc) which are modifications of the RNase Onconase (RTM) (nonc). Such novel ribonuclease molecules are highly cyclotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cyclotoxic activity compared to nonc and also lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells.
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                                               RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion; tumour cell growth; frog.
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Pred. No. 1.2e-59;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                            97WO-US002588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1997-435168/40.
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N-PSDB; AAT94959.
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                                                                                                                                  Rana pipiens
                                                                                                                                                                                     WO9731116-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY39400
                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW18224, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW06543) that
DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      have been isolated from Rana pipiens occytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy and surgery in the treaturent of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 QDWLTPQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDWLTFQKKHVTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 558; DB 2; Length 104;
Pred. No. 1.2e-59;
?; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                        EFYLSDCNVISRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R. pipiens recombinant RNase protein [Met-(-1)]rOnc.
                                                                                                                                                                                                                                                                                                                                                                                                                                Antitumour protein from Rana pipiens oocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour; chemotherapy; radiotherapy; frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 28; 45pp; English.
                                                                                                                                                                                                                                                         AAW06544 standard; protein; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US008304.
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96.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ALFA-) ALFACELL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-043063/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                        22-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9639428-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Simi
Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ardelt WJ;
                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
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AAW35123 ID AAW3 XX AC AAW3 XX XX XX XX DT 20-P

RESULT 9

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0;

0; Gaps

Length 105;

9 9

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Sequences AAW35125 to AAW35135 represent recombinant fusion proteins (rOnc) which are modifications of the RMase Onconase (RTW) (nOnc). Such novel ribonuclesse molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can stoo be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonuclesses have increased cytotoxic activity compared to nonc and also increased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 MEDWLIFQKKHITNTRDVDCDNINSTNLFHCKDKNTFIYSRPEPVKALCKGIIASKNVLT 310
                                                                                                                                                                                                               Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MQDWLTFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R. pipiens recombinant RNase ronc fusion protein 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 558; DB 2;
Pred. No. 5.8e-59;
3; Mismatches 2;
                                                                                                      Wlodawer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                           Disclosure; Page 67; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW35130 standard; protein; 358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boque L,
                                                                                                      Boque L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lower immunogenicity in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US002588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0011800P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.7%;
                   96US-0011800P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour cell growth; frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Newton DL,
                                                                                                        Newton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-435168/40.
                                                                                                                                                   WPI; 1997-435168/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT94968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 355 AA;
                                                                                                                                                                           N-PSDB; AAT94963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rana pipiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09731116-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-1996;
                   21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rybak SM,
                                                                                                           Rybak SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW35130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW35130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                         This sequence represents recombinant frog Onconase. Onconase has ribonuclease and anti-tumour activity. The CDNA was produced via PCR (using primers AAZ19769) of two synthetic DNAs whose sequences encoded most of the N-terminal or the C-terminal amino acids of mature onconase. The two PCR products generated encoded either the N-terminal 54 amino acids (minus the initial methionine) or the C-terminal 51 amino acids, and were ligated in frame at an Nrul site. The CDNA was then subcloned into a vector e.g., pBluescript, where the ATG initiation codon subcloned into a vector e.g., pBluescript, where the ATG initiation codon was ligated to the CDNA. After expression in E. coli, the recombinant crot protein was purified. The initial N-formyl methionine was cleaved off and the now N-terminal glutamate residue cyclised to form an N-terminal CC the now N-terminal glutamate residue forms part of the phosphate by proglutamate residue forms part of the phosphate collection activity. Onconase is a 12 No ribonuclease and anti-tumour activity onconase is a 12 No ribonuclease which causes cell cannous minovlving inactivation of protein synthesis by a companion in incolving inactivation of protein synthesis by a mammalian placental ribonuclease inhibitor, which may explain its cantivity against a variety of solid tumours e.g. colon or pancreatic cancers, and can be used alone or in combination with other anti-tancer agents such as tamoxifen. When used as an anti-tumour agent, Onconase can be conjugated to a marker which targets it to a specific cell type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MQDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MQDWLTFQKKHITNTKDVDCDNIMSTWLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
                                                                                                                                                                                                                             A new recombinant Onconase used to treat, e.g. colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISBEYLSDCNVISRPCKYKLKKSINIFCVICENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 558; DB 2; Length 10
Pred. No. 1.2e-59;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R. pipiens recombinant RNase rOnc fusion protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW35125 standard; protein; 355 AA
                                                                                                                  Leung S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                          Example 1; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US002588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.7%;
ilarity 95.2%;
Conservative
                       11-MAR-1998; 98US-0077557P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                  Hansen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour cell growth; frog
                                                                     (IMMU-) IMMUNOMEDICS INC
                                                                                                                                                             WPI; 1999-551416/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
ses 100; Conserv
                                                                                                                                                                                  N-PSDB; AAZ19767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 105 AA;
                                                                                                                  Goldenberg DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-FEB-1997;
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Query Match

Best Loca Matches

AAW35125;

RESULT 11 AAW35125

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Gaps

0

2; Indels

Wlodawer A;

Synthetic

Rana

Length 355;

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us-09-961-400-6.rag

(ronc) which are modifications of the RNase Onconase (RTM) (nonc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new increases have increased cytotoxic activity compared to none and also lower immunocentifit, in human human cativity compared to none and also Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells. fusion proteins (ronc) which are modifications of the RNase Onconase (RTM) recombinant Sequences AAW35125 to AAW35135 represent Disclosure; Page 72; 90pp; English lower immunogenicity in humans 

Sequence 358 AA;

09 9 1 MQDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT Gaps ·, Score 558; DB 2; Length 358; Pred. No. 5.9e-59; 3; Mismatches 2; Indels TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105 95.78; Query Match
Best Local Similarity 95.2
Matches 100; Conservative 19 19 ð g ò Dp

AAW30301 standard; protein; 104

Z

AAW30301;

(first entry) 09-JUN-1998

Recombinant onc protein

Onc; oncanase; ribonuclease; frog; antitumour; pancreatic cancer; human immunodeficiency virus type-1; HIV1; replication.

Rana pipiens

WO9738112-A1

16-OCT-1997.

97WO-US005675 04-APR-1997;

96US-00626288. 04-APR-1996;

(USSH ) US DEPT HEALTH & HUMAN SERVICES

Ardelt W; Boix E, Wu Y, Vasandani VM, Youle RJ,

WPI; 1997-512725/47.

g useful Recombinant Onc protein with glutamine residue at position 1 - useful antitumour and antiviral agent, also as cell culture selection agent.

Claim 1; Page 28; 35pp; English.

This sequence represents a recombinant Onc protein comprising a 104 amino acid sequence having Gln at position 1. Onc, a ribonuclease from Rana piptens cocytes, is known as an antitumour agent (e.g. for treating pancreatic cancer) and inhibitor of human immunodeficiency virus type-1 replication. It can be used therapeutically or as a cell-culture 

ö 61 9 2 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT Gaps t selection agent, e.g. to identify gene therapy compositions able inhibit tumour growth ; Length 104; 62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENOAPVHFVGVGHC 105 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGC 104 Indels ., Score 556; DB 2; Pred. No. 2.1e-59; 2; Mismatches 95.4%; Matches 100; Conservative Best Local Similarity Sequence 104 AA; Query Match 88833 ð 엄 ð 셤

AAB31666 standard; protein; 104 AAB31666; RESULT 14 AAB31666

AA.

(first entry) 30-APR-2001

Amino acid sequence of a frog ribonuclease protein.

Frog; ribonuclease; ranpirnase; RNase

Rana pipiens.

Location/Qualifiers Key Modified-site

/note= "this Gln is autocyclised to pyroglutamic acid" US6175003-B1 16-JAN-2001.

99US-00394268. (ALFA-) ALFACELL CORP 10-SEP-1999;

99US-00394268.

10-SEP-1999;

Saxena SK;

WPI; 2001-167808/17.

nucleic acids encoding a ribonuclease (Rnase), useful for the precise geting of Rnase to a predetermined cell receptor. targeting

Claim 1; Col 5-6; 7pp; English.

(RNase). The specification describes a synthetic ribonuclease protein, in which the addition of cysteine in the ribonuclease facilitates the chemical linking of a targeting molecule by the single reactive sulfhydryl group. The specification also describes a method for the production of rampirnase using DNA technology instead of processing biological material. The re-engineering of the protein molecule allows easier attachment to a targeting molecule thereby making it possible for the ribonuclease to be delivered to a particular cell receptor where it The present sequence represents a frog ribonuclease protein (ranpirnase) be most effective 

À, Sequence 104

Gaps Length 104; 95.4%; Score 556; DB 4; Length 10 96.2%; Pred. No. 2.1e-59; ive 2; Mismatches 2; Indels Query Match
Best Local Similarity 96.2
Matches 100; Conservative 2 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
1 ODMLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIXSRPEPVKAICKGIIASKNVLTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Constructing isolated nucleic acid encoding ribonuclease, by subjecting desired recombinant plasmid DNA to different site-directed mutations to produce nucleic acid, using different polymerase chain reaction
                                                                                                                                                                                                                                                                                                     Northern leopard frog; ranpirnase; site-directed mutation; ribonuclease.
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                                                     SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                        61 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                      Northern leopard frog ranpirnase protein.
                                                                                                                                                                       ABG32650 standard; protein; 104 AA.
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Best Local Similarity 96.2
Matches 100; Conservative
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SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENOAPVHFVGVGHC 105 

62

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Search completed: May 7, 2004, 21:38:27 Job time : 45.7895 secs

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RESULT 1
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Sequence 51, Appl
Sequence 1, Appli
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Sequence 3, Appl
Sequence 3, Appl
Sequence 61, Appli
Sequence 61, Appli
Sequence 61, Appl
Sequence 61, Appl
Sequence 64, Appl
Sequence 1, Appli
                                                                          7, 2004, 21:28:45; Search time 12.1796 Seconds (without alignments) 445.066 Million cell updates/sec
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                                                                                                                                                      1. MQDWLTFQKKGHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105
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Sequence 39,
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-875-811-39

US-08-875-811-41

US-08-875-811-51

US-09-394-268-1

US-09-687-748-1

US-09-687-748-1

US-09-675-429-1

US-08-875-811-63

US-08-875-811-63

US-08-875-811-61

US-08-875-811-61

US-08-875-811-67

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Gapop 10.0 , Gapext 0.5
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STREET: Two Embarcad
CITY: San Francisco
STATE: California
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Pred. No. 2.1e-60;
3; Mismatches 2; Indels
                                                                                                                                                                        Score 558; DB 1; Length 104; Pred. No. 2.1e-60; 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
WUMBER OF SEQUENCES: 64
CORRESPONDENTS ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew Lip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/875,811

FILING DATE: 19-FEB-1998

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: WO PCT/US97/02588

FILING DATE: 19-FEB-1997

PRIOR APPLICATION NUMBER: WO PCT/US97/02588

FILING DATE: 19-FEB-1997

PRIOR APPLICATION NUMBER: US 60/011,800

FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew Lip
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
CITY: San Francisco
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/08875811 Patent No. 6045793
                                                                                                ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
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Best Local Similarity 96.2%;
Matches 100; Conservative
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Matches 100; Conservative
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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Best Local Similarity 95.2%; Pred. No. 1e-59;
Matches 100; Conservative 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ISEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                               61 TSBFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Wlodawer, Alexander
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRELATION DATA:
CORRELATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLIASSIFICTATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INPORMATION:
NAME: FETIS, Susan K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            015280-244100US
                                                                                                                                                                                                                                                               Sequence 41, Application US/08875811 Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 355 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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us-09-961-400-6.rai

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Score 556; DB 3; L
Pred. No. 3.6e-60;
2; Mismatches 2;
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ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-687-748-1
'Sequence 1, Application US/09687748
'Patent No. 6423515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/08626288
; Patent No. 6649392
                                                                                                                  Query Match 95.4%;
Best Local Similarity 96.2%;
Matches 100; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.4%;
96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 96.2<sup>3</sup>
Matches 100; Conservative
                                   ; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-394-268-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            San Francisco
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09394268
Patent No. 617503
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
ITILE OF INVENTION:
MAKING THEM
FILLE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT APPLICATION NUMBER: US/09/394,268
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ISEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TSBFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
Sequence 51, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Middawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WG 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INPORMATION:
MAMMER: CANSON AND AND AND AND APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                     3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  015280-244100US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 358 amino acids
amino acid
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                                                                                                                                                                                                            ADDRESSEE: Townsend a STREET: Two Embarcade CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-875-811-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Sim
Matches 100;
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US-09-394-268-1
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GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION:
METHOS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
TITLE OF INVENTION: METHOS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REFERENCE: 5013 US 01
CURRENT RELIGHTON NUMBER: US/09/687,748
CURRENT RILING DATE: 1200-10-14
PRIOR PILING DATE: 1999-09-10
NUMBER: OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 1
LENGTH: 104
                                                                                                                                                    1 ODWLIFOKKHIINTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKAVLIT 60
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                                                          Gaps
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APPLICANT: Youle, Richard
APPLICANT: Youle, Richard
APPLICANT: Wo, Yon-Neng
APPLICANT: Wi, Yon-Neng
APPLICANT: Boix, Ester
APPLICANT: Ardelt, Wojeiech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Frotein Which
TITLE OF INVENTION: Allows Production by Recombinant Methods
NUMBER OF SEQUENCES: 3
Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 104;
                                                                                                                                                                                                      62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                     61 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
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                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 556, DB 4; Length 10
Pred. No. 3.6e-60;
2; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Gaps

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2 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

95.4%; Score 556; DB 4; Length 104;
Best Local Similarity 96.2%; Pred. No. 3.6e-60;
Matches 100; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Liuis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
PRILOM DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRILOM DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INPORMATION:
NAME: FRAILS, SUSAN K. 1000
NAME: FRAILS, SUSAN K. 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
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Patent No. 6045793
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 104 aming the second s
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REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEO ID NO: 32.
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-09-095-429-1
                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                    TYPE: amino s
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                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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GENERAL INFORMATION:
APPLICANT: Vorale, Richard
APPLICANT: Vasandani, Veena
APPLICANT: Was Yon-Neng
APPLICANT: Was Yon-Neng
APPLICANT: Ardelt, Wojeiech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
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TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: A MUTANT FOR OF THE WHICH
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TITLE OF INV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,429
                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,288
                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/626,288
FILING DATE: No. 6649392 yet assigned CASSIFICATION.
ATTORNEY AGENT INFORMATION:
NAME: Ran, David B. REGISTRATHON NUMBER: 38,589
REFERENCE/DOCKET NUMBER: 15280-267
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-5603
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ran, David B.
REGISTRATION NUMBER: 38,589
REFERENCE/DOCKET NUMBER: 15280-267
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-095-429-1; Sequence 1, Application US/09095429; Patent No. 6649393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 96.23
Matches 100; Conservative
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CLASSIFICATION:
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                                                                      1 MQDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                              Gaps
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Pred. No. 4.8e-60;
2; Mismatches 2; Indels
                                                                                                                                                                  61 ISEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEFYLSDCHVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 129
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                                                                                                                                                                                                                                                                                                                              Sequence 63, Application US/08875811
Patent No. 6045793
GENBRAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Hodowe, Lluis
APPLICANT: Robert Ribonuclease Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAME: Patentin Release #1.0, Version #1.30
SOCTAMES: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 15-FEB-1997
ATTOMADATE: 21-FEB-1996
ATTOMENYAGEN: 15-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Two Embarcadero Center, Eighth Floor
  Pred. No. 4e-60;
                         2; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.4%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 129 amino acids
amino acid
Best Local Similarity 95.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Faris, Susan K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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US-08-875-811-63
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1 MQDWLTFQXKHLTNTRDVDCNNIMSTNLFHCXDKNTFIYSRPEPVKAJCKGIIASKNVLT 60
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Sequence 59, Application US/08875811
Patent No. 6645793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Modawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 61, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLAI: COMPLAIS STATES OF THE STATES OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Townsend and Townsend and Crew LL
Two Embarcadero Center, Eighth Floor
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REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPRAN: (415) 576-0200
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19-FEB-1978 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
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amino acid
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Matches 100; Conservative
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CITY: San Francisco
STATE: California
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US-08-875-811-61
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251 MSDWLIFPQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPERVKALCKGIIASKNVLT 310
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Sequence 57, Application US/08875811

Fatent No. 6045793

GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Boque, Liuis
APPLICANT: Boque, Liuis
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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CIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY AGENT INFORMATION:
NUMBE: FREE: 19-FEB-1996
ATTORNEY AGENT INFORMATION:
NUMBE: FREE: SUSAN NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY AGENT INFORMATION:
NUMBE: FREE: SUSAN NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY AGENT INFORMATION:
NUMBE: FREE: SUSAN NUMBER: US 60/011,800
                                      FILING DALE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/02588

FILING DATE: 19-FEB-1997

FRIOR APPLICATION NUMBER: US 60/011,800

FILING DATE: 21-FEB-1996

ATTORING/APPLICATION NUMBER: US 60/011,800

FILING DATE: 21-FEB-1996

ATTORING/APPLICATION NUMBER: 015280-244100US

REGISTRATION NUMBER: 015280-244100US

TELECOMMUNICATION INFORMATION:

TELEPRA: (415) 576-0200

TELEPRA: (415) 576-0200

TELEPRA: (415) 576-0300

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERSTICS:

LENGTH: 355 amino acids

TYPE: amino acid

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Faris, Susan K.
REGISTRATION NUMBER: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two Embarcade
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: amino acid
; TOPDLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MQDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
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| Patent No. 6045793
| GENERAL INFORMATION:
| APPLICANT: Rybak, Susanna M. APPLICANT: Newton, Dianne L. APPLICANT: Boque, Lluis
| APPLICANT: Boque, Lluis
| APPLICANT: Boque, Lluis
| APPLICANT: Modawer, Alexander TITLE OF INVENTION: Recombinant Ribonuclease Proteins NUMBER OF SEQUENCES: 64
| NUMBER OF SEQUENCES: 64
| CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                     COMPINITY: 0.234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppd disk
COMPUTER: IBM FC compatible
CONFURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 13-FEB-1997
AND TOTAL ON NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTONIEY/AGENT INFORMATION:
AND TOTAL ON THE PARTY OF 
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COMPUTER: READLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION: PASTERN: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
ADDRESSEE: Townsend and Townsend and Crew LLP
STRERT: Two Embarcadero Center, Bighth Floor
STATE: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFRENCE/DOCKET NUMBER: 01526
TELECOMMUNICATION INFORMATION:
TELEFAK: (415) 576-0200
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 95.23
Matches 100; Conservative
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                                                                                                                                                      COUNTRY:
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Gaps

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us-09-961-400-6.rai

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1 MSDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
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                                                                                                                          Score 556; DB 3; Length 355;
Pred. No. 1.8e-59;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                     61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                        61 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 64, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Widawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVE STATES TOWNSEND AND TOWNSEND AND ADDRESSES. TOWNSEND AND ADDRESSES. TOWNSEND AND ADDRESSES TOWNSEND AND ADDRESSES STATE: TWO EDBACKED CENTER, EIGHTH Floor STATE: California COUNTRY: USA ZIP: 94111-3834

COUNTRY: USA ZIP: FLOPPY disk COMPUTER READABLE FORM:
MEDIUM TYPE: FloPPY disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/875,811
FLING DATE: 19-FEB-1998
FRIOR APPLICATION NUMBER: WO PCT/US97/02588
FRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 12-FEB-1997
FRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1997
ATORNEY/AGENT INFORMATION:
NAME: FAIS, SUSAN K.
REGEISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                          95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 64:
                                                                                                                                                Best Local Similarity 95.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                            // MOLECULE TYPE: protein
US-08-875-811-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS:
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US-08-875-811-64
                                                                                                                       Query Match
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Search completed: May 7, 2004, 21:40:43
Job time : 12.1796 secs
                  NAME/KEY: Protein
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REFERENCE/DOCKET NUMBER: 015280-244100US
TELECHMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 57;
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
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251 MSDWLFFQKKHIINTRDVDCDNIMSTNLFHCKDKNTFIXSRPEPVKAICKGIIASKNVLT 310 1 MQDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60 Gaps . 0 Query Match 95.4%; Score 556; DB 3; Length 355; Best Local Similarity 95.2%; Pred. No. 1.8e-59; Matches 100; Conservative 2; Mismatches 3; Indels 61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105 311 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355 LOCATION: 1.355 COTHER INFORMATION: /note= "R6FB[Met-(-1)]Serronc"
US-08-875-811-64

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May 7, 2004, 21:29:40 ; Search time 33.6904 Seconds (without alignments) 865.070 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                           583
1 MQDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/DCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1140673 seqs, 277566755 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                          US-09-961-400-6
                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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SUMMARIES

	Description	Seminance A avalia	, u	Semience 9 Appli	, ,	1 1	7 6	200	0 0	0 -	i:	Seguence 11, Appl	0 0	7	4,	Sequence 4, Appli	8
	ID	US-09-948-391A-6	US-09-961-400-6	US-09-961-400-9	US-09-961-400-2	US-09-948-391A-13	US-09-961-400-13	US-09-948-391A-28	US-09-961-400-28	US-09-948-391A-11	US-09-961-400-11	US-09-961-400-8	TIS-09-948-3912-2	11S - 01 - 01 - 01 - 01 - 01 - 01 - 01 -	#-WTC 040 00 0H	02-03-361-400-4	US-09-948-391A-8
		10	10	10	10	10	10	10	10	10	10	10	10	0	1 -	7	10
	Query Match Length DB	105	105	111	104	105	105	127	127	104	104	105	104	104	100	<b>*</b>	105
*	Query Match	100.0	100.0	99.5	99.1	196	99.1	99.1	99.1	98.3	98.3	97.8	97.6	97.6	0.70		96.9
	Score	583	583	580	578	578	578	578	578	573	573	570	569	569	269	) (	265
	Result No.	н	63	e	4	5	9	7	80	6	10	11	12	13	14	• (	TP

Sequence 9, Appli	Sequence 2. Appli	Segmence 1 Appli	Semience 1 Appli			Semience 3 Applia		21.	Sequence 21, Appl	22.	22,														Sequence 103. App	Segmence 6. Appli	Segmence 2. Appli	Sequence 254, App	Sequence 254, App
US-09-948-391A-9	US-10-153-882-2	US-09-986-119-1	US-09-918-887-1	US-10-461-713-53	US-09-986-119-3	US-09-918-887-3	US-09-961-400-17	US-09-948-391A-21	US-09-961-400-21	US-09-948-391A-22	US-09-961-400-22	US-09-948-391A-15	US-09-961-400-15	US-09-948-391A-26	US-09-961-400-26	US-09-948-391A-17	US-09-961-400-19	US-09-948-391A-24	US-09-961-400-24	US-09-948-391A-19	US-10-016-447-2	US-10-016-248-89	US-10-074-978A-139	US-10-016-447-5	US-10-037-417-103	US-09-286-240-6	US-09-863-777-2	US-09-731-872-254	US-09-876-997-254
10	14	σ	10	12	6	10	10	70	10	10	10	10	10	10	10	10	10	10	10	10	13	12	15	13	12	σ	σ	σ	10
111	105	104	104	104	83	83	111	111	111	117	117	110	110	111	111	111	110	110	110	110	169	119	119	124	124	147	147	147	147
6.96	96.2	94.5	94.5	94.0	76.3	76.3	49.1	48.5	48.5	48.5	48.5	48.3	48.3	48.3	48.3	48.1	47.6	47.4	47.4	46.6	27.0	25.6	25.6	22.0	21.4	19.4	19.4	19.4	19.4
265	561	551	551	548	445	445	286.5	282.5	282.5	282.5	282.5	281.5	281.5	281.5	281.5	280.5	277.5	276.5	276.5	271.5	157.5	149	149	128.5	125	113	113	113	113
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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CTHER INFORMATION: Description of Artificial Sequence:Rana pipiens of THER INFORMATION: ribonuclease with Met at position 1 (recombinant CS-09-948-391A-6
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 3.7e-59;
Matches 105; Conservative 0; Mismatches 0; Indels 0.
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                FEATURE:
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1 MODWLTFOKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIXSRDEPVKAICKGIIASKNVLT 60

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0; Gaps

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PRIOR APPLICATION NUMBER: WO PCT/US99/06641 PRIOR FILING DATE: 1999-03-26 PRIOR APPLICATION NUMBER: US 09/622,613
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PRIOR FILLING DATE: 1998-03-27
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US-09-961-400-2
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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: MEWTON, DIANNE L.
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: CT/US99/06641
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOSTUMBER: PATENTION NUMBER: CO/079,751
FRIOR FILING DATE: 1998-03-26
SEQ ID NOS: 43
SEQ ID NOS: 43
                                                                                                                                                                                                        Sequence 6, Application US/09961400

Sequence 6, Application US/09961400

Publication NO. US20030124131A1

GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: USA09961,400
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT APPLICATION NUMBER: US/09/61,400
CURRENT PILING DATE: 2001-09-25
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
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1 MQDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
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                                                TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
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100.0%; Pred. No. 3.7e-59;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 105; Conservative
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ORGANISM: Rana pipiens
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                                                                                                                                                                                                                                                      7 MQDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 66
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    Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        67 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 111
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APPLICANT: Rybak, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
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100.0%; Pred. No. 1.4e-58;
ive 0; Mismatches 0;
Score 580; DB 10;
Pred. No. 8.7e-59;
1; Mismatches 0;
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. Sequence 13, Application US/09948391A
. Publication No. US20030027311A1
. GENERAL INFORMATION:
              99.5%;
99.0%;
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Best Local Similarity 100.
Matches 104; Conservative
              Query Match
Best Local Similarity 99.03
Matches 104; Conservative
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24 QDWLTFQKKKLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Rana pipiens ribonuclease (RaPLR1) Clone 5alb cDNA; OTHER INFORMATION: insert
US-09-948-391A-28
               APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITIE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT PLIANG DATE: 2002-05-10
PRIOR PLIANG DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
PRIOR PLICATION NUMBER: W 0PCT/US99/06641
PRIOR PLICATION NUMBER: US 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
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Best Local Similarity 100.0
Matches 104; Conservative
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ORGANISM:
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Sequence 13, Application US/09961400

Publication No. US20030124131A1

GENERAL INFORMATION

APPLICANT: ROLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT APPLICATION NUMBER: US/09/25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 1909-03-26

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR PLING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-26

NUMBER OF SEQ ID NOS: 43

SECTAMBER PARENTED APPLICATION VET: 2.1
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                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens OTHER INFORMATION: ribonuclease with Met at position 1 and Gln2Ser OTHER INFORMATION: substitution (recombinant Met(-1) RaPLR1 Q1S)
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                                                                                                                                                                         ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 105
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Matches 104; Conservative
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LENGTH: 105
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                                                                                                                                                 TYPE: PRT
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Best Local S
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                                                                                                                                                                                                           FEATURE:
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99.1%; Score 578; DB 10; 100.0%; Pred. No.1.7e-58; iive 0; Mismatches 0;

Length 127;

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GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDERBERG, DAVID M.
APPLICANT: MEMORO, DIANNE L.
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE APPLICATION NUMBER: US/09/961,400
CURRENT APPLICATION NUMBER: US/082,613
FRICK PILING DATE: 2001-09-25
CURRENT APPLICATION NUMBER: DCT/US99/06641
FRICK FILING DATE: 1999-03-26
FRICK FILING DATE: 1999-03-26
FRICK FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 28
LENGHH: 127
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62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                    84 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
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100.0%; Pred. No. 1.7e-58;
tive 0; Mismatches 0;
                                                                                                                                                                            ; Sequence 28, Application US/09961400; Publication No. US20030124131A1
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US-09-961-400-28
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Best Local Similarity
Matches 104; Conserva
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Sequence 28 Application US/09948391A; Publication No. US20030027311A1; GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.; APPLICANT: Newton, Dianne L.

RESULT 7 US-09-948-391A-28

ORGANISM: Rana pipiens

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3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: CELLE
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR PELING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens; OTHER INFORMATION: ribonuclease with Gln1Ser substitution; CTHER INFORMATION: (recombinant RapLR1 Q1S)
US-09-948-391A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 104;
84 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
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APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015.280-343110US
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: W0 PCT/US99/06641
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: W0 PCT/US99/06641
PRIOR APPLICATION NUMBER: W1 09/622,613
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 69/622,613
NUMBER OF SEQ 1D NOS: 43
SOFTWARE: Patentin Ver. 2.0
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98.3%; Score 573; DB 10;
Best Local Similarity 100.0%; Pred. No. 5.1e-58;
Matches 103; Conservative 0; Mismatches 0;
                                                                                                                                                                                Sequence 11, Application US/09948391A Publication No. US20030027311A1
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) Sequence 11, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
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LENGTH: 104
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LENGTH: 104
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APPLICANT: STRAKK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: US/09/961,400
TITLE APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Newton, Diame L.
APPLICANT: Newton, Diame L.
APPLICANT: Newton, Diame L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Bepartment of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.8%; Score 570; DB 10; 1
97.1%; Pred. No. 1.1e-57;
tive 1; Mismatches 2;
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                                                         98.3%; Score 573; DB 10;
100.0%; Pred. No. 5.1e-58;
iive 0; Mismatches 0;
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
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; Publication No. US20030124131A1
; GENERAL INFORMATION:
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Best Local Similarity 97.15
Matches 102; Conservative
                                                                                     Best Local Similarity 100.
Matches 103; Conservative
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ORGANISM: Rana pipiens
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US-09-961-400-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.6%; Score 569; DB 10; Best Local Similarity 99.0%; Pred. No. 1.5e-57; Matches 103; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: ribonuclease (RaPLR1)
PRIOR FILING DATE: 1999-03-26
PRIOR PEDLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SEG ID NO 2
LENGTHARE: PATENTIN VET: 2.0
LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Rana pipiens
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US-09-948-391A-4
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RESULT 14 US-09-961-400-4

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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONUUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REPERENCE: 0.1873/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT APPLICATION NUMBER: US/09/25
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 1090-03-26
FRIOR APPLICATION NUMBER: PCT/US99/06641
FRIOR APPLICATION NUMBER: 60/079,751
FRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 4
LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens OTHER INFORMATION: ribonuclease with Met at position 1 and Met24Leu OTHER INFORMATION: substitution (recombinant Met(-1) RapLR1 Met231eu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 569; DB 10; Length 104;
Pred. No. 1.5e-57;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

96.9%; Score 565; DB 10; Length 105;
Best Local Similarity 97.1%; Pred. No. 4.3e-57;
Matches 102; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09948391A

Fublication No. US20030027311A1

GENERAL INFORMATION:

APPLICANT: Newton, Dianne I.

APPLICANT: The United States of America

APPLICANT: The United States of America

APPLICANT: The United States of America

APPLICANT: Department of Health and Human Services

TITLE OF INVENTION: Recombinant Anti-Tumor RNase

FILE REFERENCE: 015280-3431100S

CURRENT APPLICATION NUMBER: US 60/079,751

FRIOR APPLICATION NUMBER: US 60/079,751

PRIOR FILING DATE: 1999-03-27

PRIOR FILING DATE: 1999-03-27

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 43

SEC ID NOS: 43
Sequence 4, Application US/09961400 Publication No. US20030124131A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.1%;
Matches 102; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-948-391A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-948-391A-8
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Qy 61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
Db 61 TFEFYLSDCNVTSRPCKYKLKKSTITFCVTCENQAPVHFVGVGHC 105

Search completed: May 7, 2004, 21:51:56 Job time : 33.6904 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

7, 2004, 21:38:36 ; Search time 9.5276 Seconds May Run on:

(without alignments) 1060.090 Million cell updates/sec

US-09-961-400-6 583 Title: Perfect score:

1 MQDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* μακ. ......

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ			SUMMAKIES	
Result	3000	Query		í	f	
2	arose	March	rengru	. n	UL	Description
H	LO.	94.9	104	7	A39035	ribonuclease-relat
α	O	49.6	111	7	A27121	ribonuclease-relat
m	285.5	49.0	111	Н	JX0120	ribonuclease-relat
4	269.5	46.2	111	7	JX0085	pangreatic ribonuc
Ŋ	149	25.6	119	N	S41111	
9	131	22.5	124	г	NRUI	
7	128	22.0	125	Н	A32474	
00	126	21.6	128	П	NRCU	
თ	125	Н.		7	NRWHK	
10	120	20.6		-	NRKS	
11	119.5	0		Н	A35932	
12	119	20.4	128	٦	NRGPB	
13	117	20.1	124	٦	NRCB	י ט
14	116	19.9		Н	B43825	g
15	116	19.9		Н	NRYY	٠
16	114	19.6		Н	NRHP	
17	113	19.4		٦	NRHUAG	
18	112	19.2	124	Н	NRBOB	
19	112	19.2	124	1	NRPG	
20	-1	19.2	150	Н	NRBO	
21	111.5	19.1	147	7	I52489	
22	111	19.0	124	7	S08549	
23	111	19.0	128	Н	NRHO	i,
24	111	19.0	128	Н	NRPQ	pangreatic ribonic
25	111	19.0	167	~	\$20066	
26	110.5	19.0	123	٦	A43825	angiogenin - nig
27	110.5	19.0	155	C1	JC6159	- 1
28	109	18.7	124	н	NRSH	pancreatic ribonuc
29	109	18.7	124	Н	NRPRH	

pancreatic ribonuc	_	н	н	-		pancreatic ribonuc		-	۱ ۲	1 1-		۱ ۲	1 }	۱ ۲	н
NRGPA	S07141	NRWB	NRGN	NRGF	JC6160	NRDEO	NRCM	NRCMM	NRCMB	NROW2	NRHY	NRDER	NRDEN	NREKN	NRDEF
Н	7	П	7	Н	N	Н	Н	Н	Н	Н	Н	Н	Н	۲H	П
124	124	124	124	124	156	124	124	124	124	128	124	124	124	124	124
18.7	18.7	18.5	18.5	18.4	18.2	18.0	18.0	18.0	18.0	18.0	17.8	17.7	17.7	17.7	17.5
109	109	108	108	107	106	105	105	105	105	105	104	103	103	103	102
3.0	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Н	
SULT	035
ES	9

ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C;Species: Rana pipiens (northern leopard frog)
C;Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 30-Jun-1993
C;Accession: A39035
R;Ardelt, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl A;Aritle: Amino acid sequence of an anti-tumor protein from Rana pipiens occytes and earl A;Aritle: Amino acid sequence of an anti-tumor protein acid sequence of an Anti-tumor protein argument A39035
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-104 <ARD:
C;Superfamily: pancreatic ribonuclease

Gaps .. Length 104; Query Match
94.9%; Score 553; DB 2; Length 10
Best Local Similarity 95.2%; Pred. No. 1.2e-48;
Matches 99; Conservative 3; Mismatches 2; Indels

· 0

09 19

2 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT a ð

62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105 ò qq

## RESULT 2

Cibecies: Rana catesbelana (bullfrog)
Cibecies: Rana catesbelana (bullfrog)
Cibecies: Rana catesbelana (bullfrog)
Cibecies: Rana catesbelana (bullfrog)
Cibate: 19-Nov-1988 #text\_change 30-Jun-1993
Cibate: 19-Nov-1988 #text\_change 19-Nov-1988
Cibate: 19-Nov-1988

Gaps 8, Length 111; Query Match
49.6%; Score 289; DB 2; Length 11
Best Local Similarity 48.6%; Pred. No. 4.4e-22;
Matches 54; Conservative 17; Mismatches 32; Indels

3,

57 59

2 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 

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pancreatic ribonuclease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Accession: A00827
R,Beintema, J.J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1891
A,Title: Crigin of the duplicated ribonuclease gene in guinea-pig: comparison A,Reference number: A92957; MUID:87036770; PMID:6571219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ODWSSFONKHIDYPETSASNPNAYCDLMMORRNLNPTKCKTRNTFVHASPSEIQQVCGSG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
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N;Alternate names: angiogenesis factor
N;Contains: ribonuclease (EC 3.1.27..)
C;Species: Bos primigenius taurus (cattle)
C;Date: 25-Sep-1989 #sequence revision 25-Sep-1989 #text_change 15-Sep-2000
C;Accession: A32474; S02001; A30044; S48212
C;Species: Iguana iguana (common iguana)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: S41111
R;Zhao, W; Beintema, J.J.; Hofsteenge, J.
Bic. D. Biochem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonu A;Reference number: S41111; MUID:94139745; PMID:8307028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QDWLTFQKKGL-----TNTRDVDCNNIM---STNLFHCKDKNTFIXSRPEPVKAIC--K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-124 <BEI>A;Note: about one-third of the molecules lacked Ala-1
C;Comment: The cuis is a rodent belonging to the same subfamily as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 MKFQRQHMDSDGHPDTNTN--YCNEMMVRRSMTQGRCKPVNTFVHEPLEAVQAVC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Superfamily: pancreatic ribonuclease
C; Keywords: glycoprotein; hydrolase; mucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Pisulfide bonds: #status predicted
F;94/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 GIIASKNVLTTSE-FYLSDC----NVTSRPCKYKLKKSTNTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     25.6%; Score 149; DB 2; 30.7%; Pred. No. 5.7e-08; iive 19; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - cuis
                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pancreatic ribonuclease (EC 3.1.27.5) N;Alternate names: RNase 1; RNase A C;Species: Galea musteloides (cuis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35; Conservative
                                                                                                                                                                                                                                               A, Accession: S41111
A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-119 < ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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C;Species: Rana catesbeiana (bullfrog)
C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: JX0085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
J. Blochem. 106, 729-735, 1989
A;Ritle: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A;Reference number: JX0085; MUID:90130374; PMID:2613682
                                                                                                                                                                                                                                                                                                                                                                                                                K.; Kawauchi, H.; Takayanagi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eggs.
                                                                                                                                                                                                                                                                Cibonuclease-related stalic acid-binding lectin - Japanese frog C; Species: Rana japonica (Japanese frog) C; Species: Rana japonica (Japanese frog) C; Species: Rana japonica (Japanese frog) C; Date: 10. Sep-1999 #text_change 10-Sep-1999 C; Date: 10. Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C; Date: 10. Sep-1999 #text_change 10-Sep-1999 C; Date: 10. Speciesion: JX0120 Pi; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Tak, J.; Diochem. 108, 139-143, 1990 Pi; J.; Date: Japonica Japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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C;Keywords: hydrolase; pyroglucamic acid
C;I,Wodified site: pyrroglucamic acid (Gln) #status experimental
F;10,35,104/Active site: His, Lys, His #status predicted
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                         VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                   VLTTSEFYLSDC --- NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
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1e-21;
35;
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19; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.0%; Score 285.5;
llarity 45.0%; Pred. No. 1e-2
Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.2%; Score 269.5; 43.2%; Pred. No. 4e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Matches
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pancreatic ribonuclease - common iguana

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pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N.Alternate names: RNase 1, RNase A
N.Alternate names: Rase 1; RNase A
S.Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C.Species: 24.Apr-1984 #sequence_revision 24.Apr-1984 #text_change 03-Jun-1994
C.Accession: A00818
M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A.Fithe: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A.Reference number: A00818; MJID:76277855; PMID:962870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
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A;Molecule type: protein
A;Residues: 1-128 <BEL>
A;Note: residues 67-78 were positioned primarily by homology with other ribonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from African porcupine
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F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                         7 FQKKHL-----INTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 LCKNGQINCYQSNSNMHIIDCRVISNSDYPNCSYRISQBEKSIVVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Proechimys guairae (casiragua)
C.Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 30-Sep-1993
                                                                                                                                                                                                                                                                                                                                                                                    8 FEROHMDSRGSPSTNPNYCNEMMKSRNMTQGRCKPVNTFVHEPLADVQAVC----FQKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  --TISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF
                     C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; mucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110.65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas;12,41,119/Active site: His, Lys, His #status predicted;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
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C;Keywords: glycoprotein, hydrolase; nucleic acid digestion, pancreas
C;Keywords: glycoprotein, hydrolase; nucleic acid digestion, pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95;58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                         Length 128;
                                                                                                                                                                                                                                                                 36; Indels
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R;Beintema, J.J.; Knol, G.; Martena, B.
Biochim. Biophys. Acta 705, 102-10, 1982
A;Title: The primary structures of panoreatic ribonucleases
A;Reference number: A90644; MUID:83000399; PMID:7115727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                      / Match 21.6%; Score 126; DB 1;
Local Similarity 29.9%; Pred. No. 1.3e-05;
Nes 35; Conservative 18; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.4%; Score 125; DB 1; 28.6%; Pred. No. 1.5e-05; ive 15; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pancreatic ribonuclease (EC 3.1.27.5) - casiragua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: A00818
A,Molecule type: protein
A,Residues: 1-124 <EMM>
C,Superfamily: pancreatic ribonuclease
C,Keywords: glycoprotein; hydrolase; nu
F;12,41,119/Active site: His, Lys, His
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A;Residues: 1-128 <VAN>
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Best Local S
Matches 35
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Matches
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A; Reference number: A32474

A; Mccession: A32474

A; Mccession: A32474

A; Mccession: A32474

A; Mccession: A22474

A; Mccession: A22474

A; Mccession: A22474

B; Mccession: A22474

B; Mccession: B; Drotein

B; Mese; P; Damart, D: Rommens

A; Title: The complete amino acid sequence of bovine milk angiogenin.

A; Mccession: S02001; MUID:89655101; PMID:3197818

A; Mclestides: 1-125 < MME

A; Mccession: S02001

A; Mccession: S02001

A; Mccession: S02001

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Blochim. Blochka. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic A;Reference number: 490612; MUID:7706576; PMID:999896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000 C;Accession: A00822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 DEYCENMIKNRRITRPCKDRNTFIHGNXNDIKAICE----DRNGQPYRGDLRISKSEFQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence) NiAlternate names: RNase 1; RNase A C.Species: Mycastor coppus (nutria, coppu) C.Species: Apr-1984 #sequence revision 30-Sep-1988 #text change 31-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.0%; Score 128; DB 1; Length 125; 34.0%; Pred. No. 7.8e-06;
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R;Bond, M.D.; Strydom, D.J.
Biochemistry 28, 6110-6113, 1989
A;Title: Amino acid sequence of bovine angiogenin.
A;Reference number: A32474; MUID:89375344; PMID:2775757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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C;Accession: A00820
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic A;Reference number: A90612; MUID:77065676; PMID:999896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RiBond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acte 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernme
A;Reference number: S29833; MUID:93192291; PMID:8448182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pancreatic ribonuclease (EC 3.1.27.5) - Chinchilla brevicaudata (tentative sequence) N'Alternate names: Nase 1, RNase A. C.; Species: Chinchilla Norevicaudata, Chinchilla lanigera brevicaudata C; Species: Chinchilla Hequence_revision 30-Sep-1988 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                     5 LTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKALCKGIIAS 55
                                                                                                                                                                                                                                                                                                                                                 KNVL-----TTSEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAICKGIIASK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenin - rabbit
C;Species: Oryctclagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S29833; B4382S
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LITSEFYLSDCNVTSRP----CKYKLKKSTNIFCVTCENQ--APVHF
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   F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Residues: 1-124 < vAN>
A, Note: a second component of chinchilla ribonuclease has 32-Asp
C, Superfamily: pancreatic ribonuclease
C, Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F, 12, 41, 119/Active site: His, Lys, His #status predicted
F, 26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
F; 34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 124;
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                                                                                           Length 128;
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1 Similarity 31.2%; Pred. No. 0.00013;
24; Conservative 13; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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9.9e-05;
                                                                                               Score 119; DB 1;
Pred. No. 6.4e-05;
                                                                                                                                                          21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.1%; Score 117; 26.9%; Pred. No. 9
                                                                                                  20.4%;
                                                                                                                                   28.3%;
                                                                                                                                                             34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 26.9
Matches 32; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 1-125 < BON>
                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A00820
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                                                                                               Query Match
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Matches
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A; Residues: 1-145 < BON>
A; Thatrons: #status absent
C; Genetics: #status absent
C; Function: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C; Fuperfamily: pancreatic ribonuclease
C; Superfamily: pancreatic ribonuclease
C; Superfamily: pancreatic ribonuclease
C; Superfamily: pancreatic ribonuclease
C; Reyword: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F; 1-24 / Domain: signal sequence #status predicted < MIG>
F; 25-145 / Product: angiogenesis; predicted < MIG>
F; 25-145 / Product: angiogenin #status predicted < MIG>
F; 25 / Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F; 37, 64, 137 / Active site: His, Lys, His #status predicted
F; 50-104, 63-115, 81-130 / Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caria porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J. Bur. J. Biochem. 75, 91-100, 1977
Bur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig panoreatic ribonucleases. Isolation, properties, primary structure A;Reference number: A91247; MUID:77185023; PMID:862624
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                                                                                                                            7 FQKKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHLTNTRDVD------CNNIMSTNLF--HCKDKNTFIYSRPEPVKAIC--KGIIASKN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: angiogenesis factor
N;Contains: ribonuclease (EC 3.1.27.-)
C;Species: Mus musculus (house mouse)
C;Species: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                          PCKNGQSNCYESTSNMHITDCRLISNSKFPDCLYRISQEEKSIIVACEGNPYVPVHF 120
                                                                                                                                                                                       FOROHIDSSGSPSINPNYCNAMMKSRNMTOERCKPVNTFVHEPLADVQAVC----FQKNV
                                                                                                                                                                                                                                               -----LITSEFYLSDCNVTSR----PCKYKLKKSTNTFCVTCENQ--APVHF 99
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                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 17; Gaps
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                                                                    28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138
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Query Match

20.6%; Score 120; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No. 5.1e-05;
Matches 35; Conservative 18; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A35932
R;Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A;Title: Isolation and sequencing of mouse angiogenin DNA.
A;Reference number: A35932; MUID:91025023; PMID:2222458
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A;Residues: 1-128 <VAN>
A;Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digesti
F;12,41,119/Active site: His, Lys, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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Best Local Similarity 30.8%; Pred. No. 6.5e-05;
Matches 33; Conservative 12; Mismatches 45
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A, Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiogenin precursor - mouse
                                                                                                                                                                                                                                                                                                                 64
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Pancreatic ribonuclease (EC 3.1.27.5) - capybara
NyAlternate names: RNase 1; RNase A
C;Species: Hydrochaeris Nydrochaeris (capybara, carpincho)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 29-Oct-1999
C;Accession: A00824
R;Bebittema, J.G.; Neuteboom, B.
G;Mol. Evol. 19, 145-152, 1983
A;Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the ami A;Accession: A00824
A;Accession: A00824
A;Accession: A00824
A;Accession: A00824
C;Beridues: 1-128 cBEI>
C;Reywords: hydrolase; nucleic acid digestion; pancreas
C;Reywords: hydrolase; nucleic acid digestion; pancreas
C;Reywords: hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
5 LIFQKKHL-----INTRDVDCNNIMSTNLF---HCKDKNTFIYSRPEPVKAIC-KGIIAS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 KNVLTT-----SEFYLSDCNVTSR----PCKYKLKKSTNTFCVTCENQ--APVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
19.9%; Score 116; DB 1; Length 128;
Best Local Similarity 27.8%; Pred. No. 0.00013;
Matches 32; Conservative 21; Mismatches 42; Indels ;
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99 GSRNIVIACENGLPVHF 115
                                                                                               83 STNTFCVTCENOAPVHF 99
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Search completed: May 7, 2004, 21:54:53 Job time: 9.5276 secs

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OM protein - protein search, using sw model

May 7, 2004, 21:30:40 ; Search time 5.30402 Seconds (without alignments) 1030.796 Million cell updates/sec Run on:

US-09-961-400-6 583 1 MQDMLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

141681 Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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P97426 mus musculu Q29542 giraffa cam Q8wn62 saguinus oe P87350 axis porcin P80929 bos taurus P00678 cavia porce P07847 aepyceros m P00668 antilocapra P00661 ovis aries Q8wn60 saimiri sci O46529 saimiri sci P00657 bubalus bub
ECP1 MOUSE RNBR GIRCA ANGI_SAGOE RNBR AXIPR ANGZ_BOVIN RNPA_CAVPO RNPA_CAVPO RNP_ARPA RNP_SHEEP ANGI_SAISC RNS_SAISC RNS_SAISC
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## ALIGNMENTS

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CHARACTERIZATION.
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01-0CT-1989 (Rel. 12, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Ribonuclease, occytes precursor (RC 3.1.27.-) (RC-RNase) (Sialic acidbinding lectin) (SBL-C).
                                                                                                                                                                                                         QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                         QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Egg;
MEDLINE=87299649; PubMed=3304421;
Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
Titani K., Takio G., Hakomori S.;
"Amino acid sequence of sialic acid binding lectin from frog (Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue distribution, cloning, purification, cytotoxicity, and active residues for RNase activity.";
J. Biol. Chem. 273:6395-6401(1998).
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                      Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=98165825; PubMed=9497370;
Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
"The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
                                                                                                                                                                                        ;
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                                                                                                                                                                       Length 104;
                                                                                                                                                                    95.4%; Score 556; DB 1; Length 10 96.2%; Pred. No. 9.6e-53;
                                                                                                                                                                                                                                           SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                     SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                      11845 MW; 22A753C2F9E566B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION, AND SEQUENCE OF 81-101
MEDLINE=92220613; PubMed=1373237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catesbeiana) eggs.";
Biochemistry 26:2189-2194(1987).
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                      STANDARD;
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Best Local Similarity
Matches 100; Conserv
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                                                                                                                                                                                                                          MEDLINE=98437383; PubMed=9761686; Chang C.-F., Huang T.H., Chang C.-F., Chen Y.-C., How K., Huang R.-F., Huang T.H., Chang C.-F., Chen Structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullteog)..., J. Mol. Biol. 283:231-244(1998)..., J. Mol. Biol. 283:231-244(1998)..., Feferentially cleaves single-stranded RNA at pyrimidine -: FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin. It is cytotoxic against several tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00032; RNASE Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
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TISSUE=Egg;
MEDLINE=93192604; PubMed=8448385;
MILLARE-93192604. PubMed=8448385;
Mitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
Takayanagi Y., Hakomori S., Titani K.;
"Ribonuclease activity of sialic acid-binding lectin from Rana catesbeiana eggs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.1%; Score 292; DB 1; Length 133; 49.5%; Pred. No. 2.1e-24; ive 16; Mismatches 32; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF039104; AAD10702.1; -. PIR; A27121; A27121. PDB; 1BC4; 28-0CT-98. PDB; 1M07; 21-JAN-03. InterPro; IPR001427; RNaseA. PFODON; PD000535; RNaseA; 1. Prodon; PD000535; RNaseA; 1.
                                                                                                                                                 Glycobiology 3:37-45(1993).
                                                                                                                                                                                                       STRUCTURE BY NMR OF 23-133
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133 AA;
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ODWLTFOKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
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                                                                                                                                                                                             MEDLINE=91035319; PubMed=2229005;
Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
Takayanagi Y., Titani K.;
"Amino acid sequence of a lectin from Japanese frog (Rana japonica)
                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                               VLTISEFYLSDC---NVISRPCKYKLKKSINIFCVTCENQAPVHFVGVGHC 105
                                         58 VLTISEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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ProDom; PD000535; RNaseA; 1.
SMARI; SM0092; RNASe Pc; 1.
PROSTIE: PS00177; RNASE PANCEATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                               12326 MW; FDEBDDF3834ED679 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.0%; Score 285.5; DB 1
45.0%; Pred. No. 8.4e-24;
iive 19; Mismatches 35
                                                                                                     01-NOV-1990 (Rel. 16, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sialic acid-binding lectin (EC 3.1.27.-)
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InterPro; IPR001427; RNaseA.
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                                                                                       LECS RANJA
P18839;
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STANDARD;

RNPL RANCA P14626;

RNPL RANCA ID RNPL RU AC P14626

RESULT 4

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2 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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Prodom; P00074; raseA; 1.
SWART; SW00035; RNASe Pc; 1.
SWART; SW00092; RNASE PANCREATIC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 VLTISEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                        J. Biochem. 106:729-735(1989).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside: phosphatrac and 3'-phosphocligonucleotides ending in C-P or U with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family. PIR; JX0085, 7X0085.
HSSP: P11916; 1864.
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Zhao W., Beintema J.J., Hofsteenge J.;
"The amino acid sequence of iguana (Iguana iguana) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (BC 3.1.27.5) (RNase 1) (RNase A).
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01-APR-1990 (Rel. 14, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Rana catesbeiana (Bull frog).
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Eur. J. Biochem. 219:641-646(1994);
                                                                                                                                                                                                MEDLINE=90130374; PubMed=2613682;
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                                                                                                                             NCBI_TaxID=8400;
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                                                                                                                                                                                 TISSUE=Liver;
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NCBI TaxID=10090;
   26
58
12
12
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119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANGR MOUSE
064438;
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MOD_RES
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                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ODWSSFONKHIDYPETSASNPNAYCDLMMORRNLNPTKCKTRNTFVHASPSEIQQVCGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114
 -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2', 3'-cyclle phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR; 441111.
HSSP: P00656; 1LSQ.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIIASKNVLTTSE-FYLSDC----NVTSRPCKYKLKKSTNTFCVTCENQAPVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galea mustelologa (Ulis).
Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Galea.
                                                                                                                                                         InterPro; 1670074; rnaseA; 1.
PRINYS; PR0074; RNASEA; 1.
PRINYS; PR0074; RNASEA; 1.
PRODOM; PD000535; RNASE PC; 1.
PROSITE; PS00127; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
PROSITE: PROSITE ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR; A00827; NRUI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
RNASE1 OR RNS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                6072FB5B7B15BD5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.6%; Score 149; DB 1; 30.7%; Pred. No. 3.6e-09;
                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PANCREATIC; 1.
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Pfam; PR00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD0000535; RNaseA; 1.
SWART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; Hydrolase; Nuclease; Endonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                   13324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galea musteloides (Cuis)
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                                                                                                                                                                                                                                                                                                                                                          10
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91
106
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                                                                                                                                                                                                                                                                                                                                                                                                                119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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39
57
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P00680;
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RNP GALMU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 SKNV-----LITISEFYLSDCNVTSRP----CKYKLKKSINIFCVICEN--QAPVH 98
                                                                                                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SETRAIN=129, TISSUE-Liver;
MEDLINE=209, PubMed=6530072;
Brown W.E., Nobile V., Subramanian V., Shapiro R.;
Brown W.E., Nobile V., Subramanian V., Shapiro R.;
"The mouse anglogenin gene family: structures of an angiogenin-related protein gene and two pseudogenes.";
Genomics 29:200-206(1995).
-- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                             5 LIFQKKHL------TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAICKGIIA
                                                                                                                                                                                                                                                                                                                                                                                                                 6 MKFOROHMDSDGHPDTNTN--YCNEMNVRRSMTOGRCKPVNTFVHEPLEAVOAVC---S
                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
BY SIMILARITY.
MISSING (IN 1/3 OF THE MOLECULES).
W, 609C7E251A7BBA25 CRC64;
                                                                                                                                                                                                                                                                                                            32;
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PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
                                                                                                                                                                                                                                                         Length 124;
                                                                                                                                                                                                                                                                                                            34; Indels
                                                                                                                                                                                                                                                            Score 131; DB 1;
Pred. No. 3.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:104984; Angrp.
InterPro; IPR001427; RNaseA.
Ffam; PR00074; rnaseA, 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PC; 1.
Signal; Hydrolase; Nuclease; Endonuclease;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anglogenin-related protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 AA.
                                                                                                                                                                                                                                                                                                                  18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                                                           13870 MW;
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                                                                                                                                                                                                                                                              22.5%;
30.6%;
                                                                                                                                                                                                                                                                                                                  37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
     84
95
110
72
12
41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1A4Y
                                                                                                                                                                                                                124 AA;
                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primate evolution.";

Mol. Biol. Evol. 19:438-445(2002).

-1- FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity).

-1- SUBCELLULAR LOCATION: Secreted.

-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                    ---PCKYKLKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=21918422; PubMed=11919285;
Zhang J., Rosenberg H.F.;
"Diversifying selection of the tumor-growth promoter angiogenin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                              22.4%; Score 130.5; DB 1; Length 145; 38.2%; Pred. No. 4.2e-07; ive 11; Mismatches 29; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                                                                                                                                                                                                                                                                                               CKDKNTFIYSRPEPVKAIC--KGIIASKNV-LTTSEFYLSDCNVTSR-
                                                                                                                                                   29A6EB814429C4AD CRC64;
  SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
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SIMILARITY.
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     BY
BY
BY
BY
BY
37 BY
64 BY
137 BY
104 BY
115 BY
130 BY
16612 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                           123 FRYIIIGCENGWPVHF 138
                                                                                                                                                                                                                                                                                                                                                                                             84 TNTFCVTCENOAPVHF 99
                                                                                                                                                                                                                                               29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
  37
64
137
50
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81
145 AA;
                                                                                                                                                                                                                        Similarity
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DISULFID
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Best Local (
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QBWN66;
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DT 28-FEBB

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53 TWRRRHLTSP------CKDINTFIHGNRHHIKAICGDENGNPYGENLRISK 97
                                                                                                                                                  6 TPOKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIC---KGIIASKNV-LTT
                                                                                                                                23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Milk;
MEDLINE=89065101; PubMed=3197838;
Mass P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A.;
"The complete amino acid sequence of bovine milk angiogenin.";
FEBS Lett. 241:41-45(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bond M.D., Vallee B.L.;
"Isolation of bovine angiogenin using a placental ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95224057; PubMed=7708754; Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.; "Crystal structure of bovine angiogenin at 1.5-A resolution."; Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
                                                                                                      DB 1; Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning, sequencing, and expression of bovine angiogenin."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR.
MEDLINE=96280645; PubMed=8688423;
Lequin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
                                                                                                                               Indels
                                                                             27860112E85B8DF9 CRC64;
                                                                                                                                                                                                                       98 SPFQVTTCNLRGGSPRPPCQYRATRGSRNIVVGCENGLPVH 138
                                                                                                                                                                                                    62 SEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVH 98
                                                                                                                               30;
                                                                                                                  Pred. No. 4.3e-07;
                                                                                                                                                                                                                                                                                        Bond M.D., Strydom D.J.;
"Amino acid sequence of bovine angiogenin.";
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                             17; Mismatches
                                                                                                    22.4%; Score 130.5; 30.7%; Pred. No. 4.3
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MEDLINE=89375344; PubMed=2775757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89118214; PubMed=3064806;
37 BY
64 BY
138 BY
105 BY
116 BY
131 BY
1644 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibitor binding assay.";
Biochemistry 27:6282-6287(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 28:6110-6113(1989)
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Bovidae; Bovinae; Bos.
 37
64
138
50
50
63
146 AA;
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Bos taurus (Bovine).
                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 24-148.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Liver;
                                                                                                                           31;
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ANGI BOVIN
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TISSUE=Pancreas;
MEDLINE=77065676; PubMed=999896;
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셤
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                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 DVDCNNIMSTNLF--HCKDKNTFIYSRPEPVKAICKGIIASKN------VLTTSEFYL 66
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
  "Solution structure of bovine angiogenin by 1H nuclear magnetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.0%; Score 128; DB 1; Length 148; 34.0%; Pred. No. 8e-07; tive 14; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-UTL-1986 (Rel. 01, Created)
21-UTL-1986 (Rel. 01, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16969 MW; B7999124CBB523DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 TICKHKGGSSRPPCRYGATEDSRVIVVGCENGLPVHF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBLE: PSOULT, REAGE PANCHEATIC; 1.
Hydrolase; Nuclease; Endonuclease; Anglogenesis;
Protein synthesis inhibitor; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 SDC---NVTSR-PCKYKLKKSINTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANGIOGENIN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS, PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe_Pc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF135124; AAG47631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDB; 1GIO; 07-DEC-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
138
50
63
81
148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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ACT_SITE
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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Myocastor coypus (Coypu) (Nutria). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Hystricognathi, Myocastoridae;

NCBI\_TaxID=10157;

[1] SEQUENCE.

Myocastor.

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7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQKKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 L------TTSEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF 99
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. J. 157:317-323(1976).
-!-CATATYTIC ACTUATY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2',3'-cyclic phosphate intermediates.
-! SUBCENIUIAR LOCATION: Secreted.
-! TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Emmens M., Welling G.W., Beintema J.J.; "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
Balaenopteridae; Balaenoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 BY SIMILÂRITY.
95 BY SIMILARITY.
110 BY SIMILARITY.
72 BY SIMILARITY.
41 BY SIMILARITY.
119 BY SIMILARITY.
119 BY SIMILARITY.
34 N-LINKED (GLCNAC. ..).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | PROSILE; FEOULE; ANADER | PROSECULE; PROSILE; PROSILE; PROSECULED | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 126; DB 1;
Pred. No. 1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PANCREATIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=76277855; PubMed=962870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A00822; NRCU.
HSSP; P00656; 1SRN.
Interpro; 1PR001427; RNSSA.
Pfam; PF00074; rnassA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD00053; RNASSE P; 1.
PROSITE; PS00127; RNASE PC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A00818; NRWHK.
HSSP; P00656; 1SRN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribonuclease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNASE1 OR RNS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE TERRES OCCOORDES DE TERRES OCCOORDES DE TERRES DE TER
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TISSUE=Pancreas;
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64
138
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P04059;
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                                                                                                                                                ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                    SITE
                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                       Query Match
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                                                                                                         MOD_RES
                                                                                                                                                                                                                                                                     Local
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                                                                                                                                    ACT
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                                                                                                                                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                                                                                              62 NVLCKNGRINCYESNSTMHITDCRQTGSSKYPNCAXKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primate evolution.";

Mol. Biol. Evol. 19:438-445(2002).

-!- FUNCTION: May function as a tRNA specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically
                                                                                                                                                                                                                                                                                                      5 LIFQKKHLINIRDVD----CNNIMSINLF---HCKDKNTFIYSRPEPVKAICKGIIASK
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                             -----TISEFYLSDCNVISRP----CKYKLKKSINIFCVICENQ--APVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang J., Rosenberg H.F., "Diversifying selection of the tumor-growth promoter angiogenin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydrolyzing cellular tRNAs (By similarity).
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anglogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                                                                                                                                                                                                                                                Score 125; DB 1; Length 124; Pred. No. 1.4e-06;
                                                                                                                                                                                                    .) (30%).
                                                                                                                                                                                                                                                                            42; Indels
                                                                                                                                                                                                          LINKED (GLCNAC. . .) (3)
F57475459F697E20 CRC64;
                                                                              Hydrolase; Nuclease; Endonuclease; Glycoprotein.
DISULRID 26 84 BY SIMILARITY.
DISULRID 58 BY SIMILARITY.
DISULRID 65 72 BY SIMILARITY.
ACT SITE 12 12 BY SIMILARITY.
ACT SITE 41 41 BY SIMILARITY.
ACT SITE 119 119 BY SIMILARITY.
CARBOHYD 76 76 N'LINKED (GLCNAC.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 AA
                                                                                                                                                                                                                                                                           15; Mismatches
                                                                                                                                                                                                                                              Score 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
             Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
PRODOM: PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21918422; PubMed=11919285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF441667; AAL61649.1; -.
                                                                                                                                                                                                                14125 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
                                                                                                                                                                                                                                              21.48;
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                             28.68;
                                                                                                                                                                                                                                                                         34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecinae; Macaca.
                                                                                                                                                                                                                   124 AA;
                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANG OR RNASES.
                                                                                                                                                                                                                                                                                                                                                             57 NVL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MACMU
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08WN63
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
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97
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                                                                                                                                                                                                                                                                                                                                                                                           ------CKDINTFVHGNRHHITAICGDENGSPYGGNLRIST
                                                                                                                                                                                                                                                                                                                             23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proechimys guairae (Casiragua).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Hystricognathi, Echimyidae, Proechimys.
                                                                    Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid. SIGNAL 1 24 BY SIMILARITY. CHAIN 25 146 ANGIOGENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=83000399; PubMed=7115727;
Beintema J.J., Knol G., Martena B.;
"The primary structures of pancreatic ribonucleases from African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             porcupine and casiragua, two hystricomorph rodent species.";
Biochim. Biophys. Acta 705:102-110(1982).
-!-CATALYITC ACTIVITY: Bndonucleolytic cleavage to nucleoside phosphates and 3.-phosphooligonucleotides ending in C-P or with 2',3'-cyclic phosphate intermediates.
-!-SUBCELULIAR LOCATION: Secreted.
-!- SUBCRIPICITY: Palongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                              Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A)
                                                                                                                     PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                           E39A89215DB2A2A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              98 SPFQVITCKLRGGSPRPPCQYRATRGSRNIVVGCENGLPVH 138
                                                                                                                                                                                                                                                                                                                                                                                                                         62 SEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVH 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclease; Endonuclease; Glycoprotein.

May Samilarity.

May Similarity.

May Similarity.
                                                                                                                                                                                                                                                                                       20.8%; Score 121.5; DB 1; 28.7%; Pred. No. 3.9e-06;
Prodom, PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Anglogenesis;
                                                                                                                                     SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                          17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PANCREATIC; 1
                                                                                                                                                                                                                                                       16301 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00092; RNASE PC; 1
PROSITE; PS00127; RNASE_PAN
                                                                                                                                                                                                                                                                                                                        29; Conservative
                                                                                                                                                                                                                                                                                                                                                                             | :::|||:
53 TMRRRHLTSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                      24
146
25
                                                                                                                                                     37
64
138
105
116
                                                                                                                                                                                                                                                       146 AA;
                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A00821; NRKS.
HSSP; P00656; 1SRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
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malignant tissues. Abolishes protein synthesis by specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
             hydrolyzing cellular tRNAs.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                       PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                     EMBL, BC055355, AAH55355.1; -. PIR, A35932, A35932.
HSSP; P03950; 1A4Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.5%;
                                                                                                                                                                                        EMBL; U22516; AAA91366.1; -.
                                                                                                                                                                                                                                                 MGD; MGI:88022; Ang.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104
                                                                                                                                                                                                                                                                           Pfam; PF00074; rnaseA;
                                                                                                                                                                                                                                                                                                                                                                                                          25
                                                                                                                                                                                                                                                                                                                                                                                                                                      37
64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                     37
64
137
50
63
81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                           MOD RES
                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNPB_CAVPO
                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEALINE-YOR, N.A.

STRAIN-E-YORDANG. TISSUE-Liver;

KETRAINE-2388257; PubMed-12477932;

REDLINE-22388257; PubMed-12477932;

RETAUSPERGY R.L., Feeingold E.A., Gruce L.H., Derge J.G.,

RIGURER R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Halsch F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,

Rosak S.A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Ry Hillalon D.K., Muzry D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Ry Hating M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rh Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rh Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

Rh Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

Ry Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                      7 FQKKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEFVKAICKGIIASKNV 58
                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 1162:177-186(1993).

-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
to actin on the surface of endothelial cells, once bound,
anglogenin is endocytosed and translocated to the nucleus, thereby
promoting the endothelial invasiveness necessary for blood vessel
formation. Anglogenin induces vascularization of normal and
                                                                                                                                                                               64 PCKNGQSNCYESTSNMHITDCRLTSNSKFPDCLYRTSQEEKSIIVACBGNPYVPVHF 120
                                                                                                                                 FOROHIDSSGSPSTNPNYCNAMMKSRNMTQERCKPVNTFVHEPLADVQAVC----FQKNV
                                                                                                                                                             -----LITSEFYLSDCNVTSR----PCKYKLKKSINTFCVTCENQ--APVHF 99
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93192291; PubMed=8448182;
Bond M.D., Strydom D.J., Vallee B.L.;
"Characterization and sequencing of rabbit, pig and mouse
angiogenins: discernment of functionally important residues and
                                                                           28;
                                                                                                                                                                                                                                                                              01-WAY-1991 (Rel. 18, Created)
01-WAY-1991 (Rel. 18, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
ANG.
                                             Length 128;
                                                                           Indels
    34 N-LINKED (GLCNAC. . .).
14244 MW; 2DB58093A9D3C936 CRC64;
                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse angiogenin DNA . 171:988-995(1990).
                                              20.6%; Score 120; DB 1; 29.9%; Pred. No. 4.9e-06;
                                                                                                                                                                                                                                                                  145 AA.
                                                                           18; Mismatches
                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDILINE=91025023; PubMed=22222458;
BADDA M.D., Vallee B.L.,
"Isolation and sequencing of mouss Biochem. Biophys. Res. Commun. 177
                                                          29.9%;
                                                          Best Local Similarity 29.9
Matches 35; Conservative
                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
    34
128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Serum
                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regions.";
                                                                                                                                                                59
    CARBOHYD
                     SEQUENCE
                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL
                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                  ANGI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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and for commercial
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
                                                                                                                      the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 KFLTQHHDAKPKGRDDRYCERMMKRRSLTSPCKDVNTFIHGNKSNIKAICGANGSPYREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary structure and glycosidation.";

Eur. J. Biochem. 75:91-100(1977)

-i - CATALIVITC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Pancreas;
MEDLINE=77185023; PubMed=862624;
Van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastra W.,
Beintema J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL_1996 (Rel. 01, Created)
28-JUL_1996 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).
Radvia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Hystricognathi, Cavidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRMSKSPFQVTTCKHTGGSPRPPCQYRASAGFRHVVIACENGLPVHF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANGIOGENIN.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 V-LTTSEFYLSDCNVTS----RPCKYKLKKSINTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06944260BB764938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endonuclease; Anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.3e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 119.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128
                                                                                                                                                                                                                              entities requires a license agreement (St
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00092; RNASE Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angi
```

Search completed: May 7, 2004, 21:53:04 Job time : 6.30402 secs

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

OM protein - protein search, using sw model

7, 2004, 21:25:55 ; Search time 44.7895 Seconds (without alignments) 662.376 Million cell updates/sec Мау Run on:

US-09-961-400-8

584
1 MQDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 score: Title: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A Geneseq\_29Jan04:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

	•	Description	Aay28869 Recombina		Aay28866 Recombina	Aay28865 Rana pipi				Ant	Aaw35123 R. pipien	Rec	Aaw35125 R. pipien			Aab31666 Amino aci	Abg32650 Northern	굓	Aaw35134 R. pipien	ĸ.	ď	Aaw35129 R. pipien	Α.	Aaw35126 R. pipien			Aar47303 ONCONASE
SUMMARIES		OI	AAY28869	AAY28867	AAY28866	AAY28865	AAY28871	AAY28879	AAY28870	AAW06544	AAW35123	AAY39400	AAW35125	AAW35130	AAW30301	AAB31666	ABG32650	AAW35118	AAW35134	AAW35135	AAW35133	AAW35129	AAW35132	AAW35126	AAW30302	AAR12344	AAR47303
		DB	7	7	7	N	N	N	7	7	7	N	7	7	N	4	5	N	7	7	7	7	7	7	7	~	7
		Length	105	105	104	104	105	127	104	104	105	105	355	358	104	104	104	112	251	254	355	355	366	379	104	104	104
d		Match	97.9	9.76	97.1	6.7	6.7	6.7	95.9	93.3	93.3	93.3	93.3	93.3	93.0	93.0	93.0	93.0	93.0	93.0	93.0	93.0	93.0	93.0		92.5	92.5
		Score	572	570	567	565	565	565	260	545	545	545	545	545	543	543	543	543	543	543	543	543	543	543	542	540	540
	Result	No.	1	7	٣	4	īÙ	φ	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aaw00736 Protein d Aaw14065 Onconase						Aaw35116 R. pipien				Æ	į.	ď	DZ.	ď	œ.	Aaw35119 R. pipien	Aaw88234 Rana pipi	Aay33321 Frog lect
AAW00736 AAW14065	AAW06543	AAW88233	AAY33322	AAB31667	ABG31617	AAW35116	AAW35122	AAW35117	AAW35115	AAW18224	AAW35127	AAW35131	AAW35120	AAW35128	AAW35121	AAW35119	AAW88234	AAY33321
0 0	7	N	N	4	Ŋ	7	7	N	7	7	7	~	N	~	~	7	7	7
104	104	104	104	104	104	105	106	107	105	104	358	365	107	360	111	83	83	111
92.5	92.5	92.5	92.5	92.5	92.5	92.1	92.1	92.1	92.0	91.6	91.4	91.4	88.2	82.5	90.6	74.0	74.0	48.5
540	540	540	540	540	540	538	538	538	537	535	534	534	515	482	470.5	432	432	283
26	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

RESULT 1

Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein. AAY28869 standard; protein; 105 AA. 25-JAN-2000 (first entry) AAY28869; AAY28869 

Recombinant Met(-1) Rana pipiens ribonuclease Met21Leu-(His)6; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase; cancercus B cell, Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease.

Rana pipiens. Synthetic.

Location/Qualifiers

'note= "Met not found in wild type RaPLR1" Key Misc-difference

/note= "(His)6 histidine tag attached to N-terminal Met" /note= "Wild type Met replaced with Leu" Misc-difference 24 Misc-difference 1

WO9950398-A2

07-OCT-1999

99WO-US006641. 26-MAR-1999; 98US-0079751P. 27-MAR-1998; (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Rybak SM, Newton DL;

WPI; 1999-610847/52.

N-PSDB; AAZ08127.

for e.g. New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.

Claim 4; Page 59; 71pp; English.

The present sequence is a recombinant Rana pipiens ribonuclease protein

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(RaPLRI) with Met at position 1 attached to (His)6 tag and Met24Leu. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with used for treatment of cancer and autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant Met(-1) Rana pipiens ribonuclease; RapLR1; CD22; RNase; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                                                                                                                                      MQDWLIFQKKHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                                                                                                                                                                                                                                              MQDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                                                                                                                                                                                                   Gaps
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                                                                                                                                                                        DB 2; Length 105;
                                                                                                                                                                                                                                                                      TFEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                        note= "Met not found in wild type RaPLRI"
                                                                                                                                                                                                 2; Indels
                                                                                                                                                                      Score 572; DB 2,
Pred. No. 8e-63;
                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                               AAY28867 standard; protein; 105 AA
                                                                                                                                                                       97.9%;
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                                                                                                                                                                                           Matches 103; Conservative
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                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease.
                                                                                                                                           Sequence 105 AA;
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                                                                                                                                                                      Query Match
                                                                                                                                                                                  Local
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The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Met at position 1. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic

New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.

WPI; 1999-610847/52.

N-PSDB; AAZ08126

71pp; English.

Claim 34; Page 57;

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          sarcoma cells. Recombinant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein with Met23Leu. Carboxy terminal end of recombinant RaphRi has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by
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gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinan ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moleties to form cyclotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
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                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                            0;
                                                                                                                                                                             Length 105;
                                                                                                                                                                                                                                                                                                                              TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVFFVGVGHC 105
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treating cancers, viral infections or autoimmune diseases.
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                                                                                                                                               Score 570; DB 2; Leng
bred. No. 1.4e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant RaPLR1 Met23Leu amino acid sequence.
                                                                                                                                                                                                          1; Mismatches
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                                                                                                                                                                         97.6%;
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                                                                                                                                                                                                     102; Conservative
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                                                                                                                                                                      Query Match
Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disease
                                                                                                                                        Sequence 105 AA;
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                                                                                                                                                                                                                09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog; human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
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                                                                                                                 Length 104;
                                                                                                                                                                                                                                               62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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Pred. No. 3.3e-62;
                                                                                                                                                0; Mismatches
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                                                                                                                 97.1%;
98.1%;
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                                                                                                                                                102; Conservative
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                                                                                                              Query Match
Best Local Similarity
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                                                                                 Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9950398-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pipiens
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                                                                                                                                                                                                                                                                                                                                                                                                AAY28865;
                                                diseases
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The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-
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                 1 ODWITFOKKHITNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTF1YSRPEPVKA1CKG11ASKNVLTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Met not found in wild type RaPLR1"
                                                               62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                                                                           Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.
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Matches 101; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                           pipiens.
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Query Match
96.7%; Score 565; DB 2; Length 104;
Best Local Similarity 97.1%; Pred. No. 5.9e-62;
Matches 101; Conservative 1; Mismatches 2; Indels

Sequence 104 AA;

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Synthetic.
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Best Local S
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                                                                                                                                                             RESULT 7
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                                                                                                                                                                                                              The present sequence is a Rana pipiens Clone 5alb ribonuclease (RaPLRI). It is encoded by Clone 5alb cDNA obtained from Rana pipiens liver mRNA library. It exhibits differences with Oncoase (FTM) at amino acid residues 11, 20, 85 and 103. Carboxy terminal end of RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody glarected against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cyclockic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                 Rana pipiens ribonuclease Clone 5alb; RaPLR1; covalently bound; RNase; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase; Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer; recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
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                MQDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
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/label= Rana_pipiens_Clone_5alb_ribonuclease
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Pred. No. 7.6e-62;
1; Mismatches 2; Indels
                                                                105
                                                             TFEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                         TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .23
/label= Signal peptide
/note= "Putative"
24. .127
                                                                                                                                                                                                                                                                      Rana pipiens Clone 5alb ribonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 69; 71pp; English.
                                                                                                                                                                            Ą.
                                                                                                                                                                           AAY28879 standard; protein; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US006641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0079751P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.78;
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-610847/52.
N-PSDB; AAZ08136.
                                                                                                                                                                                                                                                                                                                                                                   autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9950398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1998;
                                                                                                                                                                                                                                       25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rybak SM,
                                                                                                                                                                                                         AAY28879;
                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                             RESULT 6
                                                                                                                                                          AAY28879
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Gaps

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Conservative

Best Local Similarity Matches 101; Conserv

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
61
                                 24 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKALCKGIIASKNVLTT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant Rana pipiens ribonuclease, RaPLRI GlnISer; covalently bound; Liz antibody, Ilagand binding molety, CD22, cancerous B cell, frog, Kaposi's sarcoma; human chorionic gonadotrophin; hGG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
ODWLTFOKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 DWLTPQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.9%; Score 560; DB 2; Length 104; 97.1%; Pred. No. 2.4e-61; Live 1; Mismatches 2; Indels
                                                                                                                                105
                                                                                                                                                                                         SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENGAPVHFVGVGHC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant RaPLR1 Gln1Ser amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSE ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               A.
                                                                                                                            FEFYLSDCNATSRPCKYKLKKSTNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 34; Page 60; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                           AAY28870 standard; protein; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US006641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ08128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9950398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-2000
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Wlodawer A;

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AAW35115 to AAW35123 encode recombinant proteins (rOnc) which are modifications of the RNase Onconase (RTW) (nOnc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used increased cytotoxic activity compared to nonc and also lower immunogenicity in humans
                                                                                                                                                                                                                                                                                      Ribonuclease molecules based on native Onconase - used for killing cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MQDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                      ribonuclease; cytotoxic; onconase; nonc; immunofusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribonuclease; protein synthesis; inhibition; cancer; cytotoxic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TFEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.3%; Score 545; DB 2; 92.4%; Pred. No. 1.8e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                              Disclosure; Page 65-66; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY39400 standard; protein; 105 AA.
                                                                                                                                                                                                                        Boque L,
                                                                                                                                           97WO-US002588
                                                                                                                                                                    96US-0011800P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US004252.
                                                                                                                                                                                                                                                                                                      tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant frog Onconase
                                    cell growth; frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                       Newton DL,
                                                                                                                                                                                                                                               WPI; 1997-435168/40.
N-PSDB; AAT94959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
hes 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 105 AA;
                                                             Rana pipiens
                                                                                    WO9731116-A2.
                                                                                                                                           19-FEB-1997;
                                                                                                                                                                                                                                                                                                      particularly
                                                                                                               28-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9946389-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1999
                                                                                                                                                                                                                       Rybak SM,
                       RNase A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                    tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
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         셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW18224, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW06543) that have been isolated from Rana pipiens occytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy and surgery in the
DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QDWLIFQKKHLINIRDVDCNNILSINLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 545; DB 2; Length 104;
Pred. No. 1.8e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104
                                                  EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R. pipiens recombinant RNase protein [Met-(-1)]rOnc.
                                                                                                                                                                                                  Antitumour protein from Rana pipiens oocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                           Tumour; chemotherapy; radiotherapy; frog
                                                                                                                  AAW06544 standard; protein; 104 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW35123 standard; protein; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                     96WO-US008304.
                                                                                                                                                                                                                                                                                                                                                              95US-00467955
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                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       (ALFA-) ALFACELL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-043063/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 104 AA;
                                                                                                                                                                                                                                                       Rana pipiens
                                                                                                                                                                                                                                                                                WO9639428-A1
                                                                                                                                                                                                                                                                                                                                     03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                        22-AUG-1997
                                                                                                                                                                                                                                                                                                         12-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                 Ardelt WJ;
                                                   62
                           63
                                                                                                                                               AAW06544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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Matches
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ID AAW3

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AC AAW3

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Length 105;

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                     This sequence represents recombinant frog Onconase. Onconase has ribonuclease and anti-tumour activity. The CDNA was produced via PCR (using primers AAZ19769) of two synthetic DNAS whose sequences encoded most of the N-terminal or the C-terminal amino acids (minus the initial methionine) or the C-terminal 54 amino acids (minus the initial methionine) or the C-terminal 51 amino acids, and were ligated in frame at an Nrul site. The CDNA was then subcloned into a vector e.g., pBluescript, where the ATG initiation codon subcloned into a vector e.g., pBluescript, where the ATG initiation codon subcloned into a vector e.g., pBluescript, where the ATG initiation codon to the CDNA. After expression in E. coli, into recombinant crot protein was purified. The initial N-formyl methionine was cleaved off and the now N-terminal glutamate residue cyclised to form an N-terminal glutamate residue cyclised to form an N-terminal compassion in E. coli, the recombinant of the phosphate of phosphate by proglutamate is als North color both ribonuclease and anticumour activity. Onconase is a 12 No ribonuclease which causes cell death as a result of potent inhibition of protein synthesis by a mechanism involving inactivation of collular RNA. It is not inhibited by mammalian placental ribonuclease inhibitor, which may explain its continuity against a variety of solid tumours e.g. colon or pancreatic cancers, and can be used alone or in combination with other anti-cancer agents such as tamoxifen. When used as an anti-tumour agent, Onconase can be conjugated to a marker which targets it to a specific cell type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MQDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MODWLIFOXKHITUTKDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNase A; ribonuclease, cytotoxic, onconase, nOnc; immunofusion; tumour cell growth; frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                        A new recombinant Onconase used to treat, e.g. colon cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TFEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 545; DB 2; Length 10
Pred. No. 1.8e-59;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R. pipiens recombinant RNase rOnc fusion protein 1.
                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW35125 standard; protein; 355
                                                                                                                                                                  Example 1; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US002588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.3%;
ilarity 92.4%;
Conservative
              98US-0077557P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                    Hansen H,
                                         (IMMU-) IMMUNOMEDICS INC
                                                                                                WPI; 1999-551416/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                             N-PSDB; AAZ19767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 105 AA;
                                                                   Goldenberg DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rana pipiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9731116-A2
              11-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW35125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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Sequences AAW35125 to AAW35135 represent recombinant fusion proteins (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such movel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nonc and also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 MEDWLIFPQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 310
                                                                                                                                                                                                                                Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MQDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TFEFYLSDCNATSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R. pipiens recombinant RNase ronc fusion protein 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 545; DB 2;
Pred. No. 8.9e-59;
4; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wlodawer A;
                                                                                                      Wlodawer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                          Disclosure; Page 67; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW35130 standard; protein; 358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boque L,
                                                                                                      Boque L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lower immunogenicity in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0011800P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US002588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.3%;
96US-0011800P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour cell growth; frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rybak SM, Newton DL,
                                                                                                      Newton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-435168/40.
N-PSDB; AAT94968.
                                                                                                                                                           WPI; 1997-435168/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                     N-PSDB; AAT94963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9731116-A2
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21-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                        Rybak SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW35130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nonc and also
                                                                    Ribonuclease molecules based on native Onconase - used for killing cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ribonuclease moderates are highly cytotoxic and can be used alone form chemical continues or to the continues or the continues or to the continues
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences AAW35125 to AAW35135 represent (rOnc) which are modifications of the RNa
                                                                                                                                                                                                                                                                                           Disclosure; Page 72; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lower immunogenicity in humans
                                                                                                                                                         particularly tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 358 AA;
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recombinant fusion proteins

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                                                   1 MQDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                        Gaps
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  Score 545; DB 2; Length 358;
Pred. No. 9e-59;
                                                                                TFEFYLSDCNATSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 105
                                                                                           4; Indels
                      4; Mismatches
93.3%;
          Best_Local Similarity 92.4
Matches 97; Conservative
                                                                                61
                                                                                                    61
 Query Match
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RESULT 13

AAW30301 standard; protein; 104 AA 09-JUN-1998 AAW30301; 

(first entry) Recombinant onc protein

Onc; oncanase; ribonuclease; frog; antitumour; pancreatic cancer; human immunodeficiency virus type-1; HIV1; replication.

Rana pipiens

WO9738112-A1

16-OCT-1997.

97WO-US005675. 04-APR-1997; 96US-00626288 04-APR-1996; (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Ardelt W; Boix E, Wu Y, Youle RJ, Vasandani VM,

WPI; 1997-512725/47.

as - nseful Recombinant Onc protein with glutamine residue at position 1 - antitumour and antiviral agent, also as cell culture selection

Claim 1; Page 28; 35pp; English

This sequence represents a recombinant Onc protein comprising a 104 amino acid sequence having Gln at position 1. Onc, a ribonuclease from Rana pipiens cocytes, is known as an antitumour agent (e.g. for treating pancreatic cancer) and inhibitor of human immunodeficiency virus type-1 replication. It can be used therapeutically or as a cell-culture

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                                                                             61
                                                                                             09
                                                                                                                                                                                                                                                                                        1
/note= "this Gln is autocyclised to pyroglutamic acid"
                                                                           2 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                    1 QDWLTFQKKHITNTRBVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                           Gaps
  to
selection agent, e.g. to identify gene therapy compositions able inhibit tumour growth
                                                            .,
                                          Length 104;
                                                                                                            62 PEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                        61 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                           Indels
                                                                                                                                                                                                                          Amino acid sequence of a frog ribonuclease protein.
                                                            4
                                        Score 543; DB 2;
Pred. No. 3.2e-59;
3; Mismatches 4
                                                                                                                                                                                                                                           Frog; ribonuclease; ranpirnase; RNase
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                         Ą
                                                                                                                                                                       AAB31666 standard; protein; 104
                                                                                                                                                                                                                                                                                                                                                 99US-00394268.
                                                                                                                                                                                                                                                                                                                                                                  99US-00394268,
                                         93.0%;
93.3%;
                               Query Match
Best Local Similarity 93.50,
These 97, Conservative
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  (ALFA-) ALFACELL CORP
                         Sequence 104 AA;
                                                                                                                                                                                                                                                                             Key
Modified-site
                                                                                                                                                                                                                                                             Rana pipiens
                                                                                                                                                                                                                                                                                                               US6175003-B1
                                                                                                                                                                                                                                                                                                                                                10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                 10-SEP-1999;
                                                                                                                                                                                                          30-APR-2001
                                                                                                                                                                                                                                                                                                                                16-JAN-2001.
                                                                                                                                                                                        AAB31666;
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                                                                                                                                                       RESULT
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ö The present sequence represents a frog ribonuclease protein (ranpirnase) (RNase). The specification describes a synthetic ribonuclease protein, in which the addition of cysteine in the ribonuclease facilitates the chemical linking of a targetine molecule by the single reactive sulfhydryl group. The specification also describes a method for the production of ranpirnase using DNA technology instead of processing biological material. The re-engineering of the protein molecule allows easier attachment to a targeting molecule thereby making it possible for the ribonuclease to be delivered to a particular cell receptor where it Gaps Length 104; 93.0%; Score 543; DB 4; Length 10 93.3%; Pred. No. 3.2e-59; ive 3; Mismatches 4; Indels 97; Conservative might be most effective Similarity Sequence 104 AA; Query Match Best Local S: Matches 97

New nucleic acids encoding a ribonuclease (Rnase), useful for the precise targeting of Rnase to a predetermined cell receptor.

English.

Claim 1; Col 5-6; 7pp;

WPI; 2001-167808/17.

Saxena SK;

2 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a new method of constructing isolated nucleic acid encoding ribonuclease protein with N-terminal Met at position -1 and Glu at position 1, where its Met has been cleaved and its Glu has been autocyclised. The method of the invention involves subjecting pETIId-ronc(QI,M23L) plasmid DNA to two different site-directed mutations, each using overlapping PCR protocol. The method is useful for constructing an isolated nucleic acid encoding the ribonuclease. The present amino acid sequence represents the northern leopard frog rampirnase protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
Northern leopard frog; ranpirnase; site-directed mutation; ribonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Constructing isolated nucleic acid encoding ribonuclease, by subjecting desired recombinant plasmid DNA to different site-directed mutations to produce nucleic acid, using different polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.0%; Score 543; DB 5; Length 104; Best Local Similarity 93.3%; Pred. No. 3.2e-59; Matches 97; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                  62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                      61 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                              Northern leopard frog ranpirnase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: May 7, 2004, 21:38:27 Job time: 44.7895 secs
                                                                                                                                                                           ABG32650 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Col 5-6; 8pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-OCT-2000; 2000US-00687748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00394268
                                                                                                                                                                                                                                            15-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ALFA-) ALFACELL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-664633/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                US6423515-B1.
                                                                                                                                                                                                                                                                                                                                                   Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saxena SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                           ABG32650;
                                                                                                                                     RESULT 15
ABG32650
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
TELEFAX: No. 5728805 Applicable
TELEX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Applisequence 39, Applesquence 41, Applisequence 1, Applisequence 1, Applisequence 1, Applisequence 1, Applisequence 32, Applesquence 63, Applesquence 64, Applesquence 65, Applesque
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Sequence 1, Appli
Sequence 1, Appli
Sequence 13, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                   7, 2004, 21:28:45 ; Search time 12.1796 Seconds (without alignments) 445.066 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                             1 MQDWLTFQKKHLTNTRDVDC......TFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/6B_COMB.pep;*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-875-811-39
US-08-875-811-41
US-08-875-811-41
US-09-874-268-1
US-09-687-748-1
US-09-687-811-62
US-08-875-811-63
US-08-875-811-63
US-08-875-811-63
US-08-875-811-63
US-08-875-811-64
US-08-875-811-65
US-08-875-811-64
US-08-875-811-13
US-08-875-811-13
US-08-875-811-13
US-08-875-811-13
US-08-875-811-13
                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                  389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listing first 45 summaries
                                                                             - protein search, using sw model
                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Score Match Length
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                                                                                                                                                                                                                          Perfect score:
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                                                                                                                     Run on:
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104 105 105 107 107 107 358 360 111 83 83 83 111 111 111 114 1114	cation US/ is TON: TON: TON: PH.DY: TENCES: ADDRESS: ADDRESS: ADDRESS: N. BOX H. JF.	". Jersey ". Jersey ". Jersey ". 1933 ". Formal State Formation of the for	13-NOV-1989 ON DATA: UMBER: US 07/814, UMBER: US 08/283, ON DATR: UMBER: US 08/283, ON DATR: UMBER: US 08/283, INFORMATION: IATK H. NUMBER: 27507 NUMBER: 27507 NUMBER: SO77
00000000000000000000000000000000000000	2 Application 728805 'ORMATION: 'E Ardelt Ph. INVENTION: SEQUENCES: IDENCE ADDRES: IDENCE ADDRES: F.O. BOX E P.O. BOX E P.O. BOX E NORT HILLS	USA  USA  USA  USA  078-0383  078-0383  CABLABLE FO  E IBM PC  IS SYSTEM:  IS PATENTION  ION NUMBER	DATE: 13-W TICATION DA TICATION DA TITION NUMBER DATE: 03-F TION NUMBER DATE: 01-A AGEN TINFORI JAY, MARK H AATION NUMBE AATION NUMBE AATION NUMBE
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                                                                                                                                                    61 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
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                                                                                                                                                                                                                                                         Sequence 41, Application US/08875811
Fatent No. 6045793
GENERAL INFORMATION:
APPLICANT: Newton, Dianne L.
APPLICANT: Modawer, Alexandar
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
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CURRENT APPLICATION DATE:
PALLOATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INPORMATION:
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INFORMATION FOR SEQ ID NO: 4
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US-08-875-811-41
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US-08-875-811-51
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                                                                                                                                                                                            93.3%; Score 545; DB 1; Length 104; 93.3%; Pred. No. 9.3e-59;
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                                                                                                                                                                                                                                        Indels
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Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Boque, Lluis
APPLICANT: Moddawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMFUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LIP
STREET: Two Embarcadero Center, Eighth Floor
TTT: San Francisco
STATE: California
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REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                        3; Mismatches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
           HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: OCC
                                                            N-terminal
                                                                                                                                                                                                                                      97; Conservative
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protein
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Matches 97; Conserv
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ZIP: 94111-3834
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APPLICANT: Youle, Richard APPLICANT: Vasandani, Veena
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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SEQ ID NO 1
LENGTH: 104
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California
                           ; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-394-268-1
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                                                                                                           Query Match
Best Local Similarity
Matches 97; Conserv
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STATE:
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APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
TITLE OF INVENTION: MAKING THEM
TITLE OF INVENTION MAKING THEM
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
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APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 545; DB 3; Length 358;
Pred. No. 4.6e-58;
4; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-LOOS/MS-DOOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INPORMATION:
NAME: Frais, Susan K.
REFERENCE/DOCKET NUMBER: 015280-244100US
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
      Sequence 51, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Saxena, Shallendra K
APPLICANT: Saxena, Shallendra K
TITLE OF INVANTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REFERENCE: 5013 US 01
CURRENT APPLICATION NUMBER: US/09/687,748
PRIOR APPLICATION NUMBER: 09/394,268
PRIOR PELING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                           1 QDWLIFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPBPVKAICKGIIASKNVLTT
                                                                                                                        2 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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APPLICANT: Boix, Ester
APPLICANT: Ardelt, Woeiech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Frotein Which
TITLE OF INVENTION: Allows Production by Recombinant Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
93.0%; Score 543; DB 4; Length 104;
Best Local Similarity 93.3%; Pred. No. 1.6e-58;
Matches 97; Conservative 3; Mismatches 4; Indels
Length 104;
                                                                                                                                                                                                                                                                                   61 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
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                                                               4; Indels
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93.0%; Score 543; DB 3;
93.3%; Pred. No. 1.6e-58;
live 3; Mismatches 4;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09687748
Patent No. 6423515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-626-288-1
; Sequence 1, Application US/08626288
; Patent No. 6649392
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1 QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                            2 ODWLIFQKKHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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                                                                                                                                                                                                                                                            Score 543; DB 4; Length 104;
Pred. No. 1.6e-58;
3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALING DATE: 19-FEB.1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB.1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             015280-244100US
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19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32, Application US/08875811
Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: FAIIS, SUSAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELBFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 32:
       (415) 543-9600
                                                                                                                                                                                                                                                            Query Match 93.0%;
Best Local Similarity 93.3%;
Matches 97; Conservative
                      TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                               LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 112 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-095-429-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-875-811-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
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       TELEPHONE:
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US-08-875-811-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
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APPLICANT: Youle, Richard
APPLICANT: Wu you-Neng
APPLICANT: Boix, Ester
APPLICANT: Ardelt, Wojeisch
IITLE OF INVENTION: A Mattant Form of Cytocoxic Protein Which
IITLE OF INVENTION: Allows Production by Recombinant Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.0%; Score 543; DB 4; Length 104; Best Local Similarity 93.3%; Pred. No. 1.6e-58; Matches 97; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CARENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,288
FILING DATE: No. 6649392 yet assigned
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: Callfornia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,429
                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Ran, David B.
REGISTATION NUMBER: 15280-267
REFERENCE/DOCKET NUMBER: 15280-267
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 15280-267
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09095429 Patent No. 6649393
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REGISTRATION NUMBER: 38,589
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                                                                                                                                                                                                                                                                                                                                                                               104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-626-288-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend &
STREET: One Market PJ
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                             LENGIH:
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1 MQDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
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                                                                                                                        8 MSDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 67
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                                                                                                                                                                                            61 TFEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 129
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                                         Indels
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                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
1.8e-58;
5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      015280-244100US

 Mismatches

                     Pred. No. 1.8e
3; Mismatches
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FILING DATE: 21-FEB-1996
ATORING DATE: 21-FEB-1996
ATORING DATE: 31-FEB-1996
ATORING NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-2441
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFENCE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           Sequence 63, Application US/08875811
Patent No. 6045793
                     92.4%;
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amino acid
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                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 97; Conserv
                 Best Local Similarity
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US-08-875-811-63
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                                         Matches
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147 MSDWLIFQKKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 206
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                                                             GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodwer, Alexander
ITILE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.0%; Score 543; DB 3; L.
92.4%; Pred. No. 5.1e-58;
" wiematches 5;
                                                                                                                                                                                                                                                   Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                         Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                     Sequence 59, Application US/08875811
Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 61, Application US/08875811; Patent No. 6045793; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 59: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 251 amino acids
amino acid
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Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
US-08-875-811-59
                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-875-811-59
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                                                                                                                                                                                                                                                                         STREET:
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NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              : 355 amino acids
amino acid
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Best Local Similarity 92.4%
----hes 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Faris, Susan K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-875-811-49
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USA
                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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US-08-875-811-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.0%; Score 543; DB 3; Length 254; 92.4%; Pred. No. 5.2e-58; ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TFEFYLSDCNATSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49, Application US/08875811
Patent No. 6045793
GRNERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bordue, Liuis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/875,811 FILING DATE: 19-FEB-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Bighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       015280-244100US
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FRIENG APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                      ZIP: 94111-3834
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Faris, Susan K. REGISTRATION NUMBER: 01,739 REFERENCE/DOCKET NUMBER: 01 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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Matches 97; Conservative
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ZIP: 94111-3834
COMPUTER READABLE FORM:
                                                                California
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                                                                                       COUNTRY:
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251 MSDWLIFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 310
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Pred. No. 8e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CIIY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER, TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC Comparible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                 . 41,739
.ep.: 015280-244100US
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02589
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
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APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEBB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/011,800 FILING DATE: 21-FEB-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 57, Application US/08875811; Patent No. 6045793
                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
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92.4%;
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Page 7

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1 MQDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 64, Application US/08875811
| Patent No. 6045793
| GENERAL INFORMATION:
| APPLICANT: Rybak, Susanna M. |
| APPLICANT: Rybak, Lluis
| APPLICANT: Boque, Lluis
| APPLICANT: Boque, Lluis
| APPLICANT: Modawer, Alexander
| TITLE OF INVENTION: Recombinant Ribonuclease Proteins
| NUMBER OF SEQUENCES: 64
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Two Embarcadero Center, Bighth Floor
| CITY: San Francisco
| STREF: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION OPER: 19-FEB-1998
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 1-19-FEB-1997
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Shaan K,
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELEFORMULICATION NUMBER: 015280-244100US
TELEFORMULICATION NUMBER: 015580-244100US
TELEFORMULICATION NUMBER: 015580-244100US
TELEFORMULICATION NUMBER: 015580-244100US
TELEFORMULICATION NUMBER: 015580-244100US
TELEFORMULICATION OF 64:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
CHAR
           015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                  : 355 amino acids
amino acid
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 92.4
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-57
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-875-811-64
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                                                                                                                                                  0; Gaps
                                                                                                         Length 355;
                                                                                                                                                                                                                                                                                                311 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355
                                                                                                                                                                                                                                                                       61 TFEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                       Score 543; DB 3; Length 35:
Pred. No. 8e-58;
3; Mismatches 5; Indels
; NAME/KEY: Protein
; LOGATION: 1..355
; OTHER INFORMATION: /note= "E6FB[Met-(-1)]SerrOng"
US-08-875-811-6
                                                                                                         93.0%;
92.4%;
                                                                                                       Query Match
Best Local Similarity 92.4
Matches 97; Conservative
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Search completed: May 7, 2004, 21:40:44 Job time: 13:1796 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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May 7, 2004, 21:29:40 ; Search time 33.6904 Seconds (without alignments) 865.070 Million cell updates/sec US-09-961-400-8 584 1 MQDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 OM protein - protein search, using sw model Title: Perfect score: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1140673 segs, 277566755 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Sequence 8, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 9, Appli	Sequence 8, Appli	Sequence 9, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 13, Appl	Sequence 13, Appl	Sequence 28, Appl	Sequence 28, Appl	Sequence 11, Appl	Sequence 11, Appl
ΩΙ	US-09-961-400-8	US-09-948-391A-4	US-09-961-400-4	US-09-961-400-9	US-09-948-391A-8	US-09-948-391A-9	US-09-948-391A-6	US-09-961-400-6	US-09-961-400-2	US-09-948-391A-13	US-09-961-400-13	US-09-948-391A-28	US-09-961-400-28	US-09-948-391A-11	US-09-961-400-11
1	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
% Query Match Length DB	105	104	104	111	105	111	105	105	104	105	105	127	127	104	104
% Query Match	100.0	98.5	98.5	97.9	97.8	97.8	97.6	97.6	96.7	96.7	96.7	96.7	96.7	95.9	95.9
Score	584	575	575	572	571	571	570	570	565	292	265	565	565	260	260
Result No.	1	2	æ	4	2	9	7	80	σ	10	11	12	13	14	15

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Sequence 2, Appli Sequence 2, Appli	- H	Sequence 53, Appl	Sequence 3, Appli	Sequence 3, Appli	21,			Sequence 22, Appl	17,	Sequence 19, Appl	15,	Sequence 15, Appl	Sequence 26, Appl	26,	17,	Sequence 19, Appl	Sequence 24, Appl	24,	2,1	89, 7	139	Sequence 5, Appli	Sequence 103, App	Sequence 8, Appli	Sequence 50, Appl	Sequence 57, Appl	Sequence 6, Appli
10 US-09-948-391A-2 14 US-10-153-882-2	9 US-09-388-113-1 10 US-09-918-887-1	12 US-10-461-713-53	9 US-09-986-119-3	10 US-09-918-887-3	10 US-09-948-391A-21	10 US-09-961-400-21	10 US-09-948-391A-22	10 US-09-961-400-22	10 US-09-961-400-17	10 US-09-961-400-19	10 US-09-948-391A-15	10 US-09-961-400-15	10 US-09-948-391A-26	10 US-09-961-400-26	10 US-09-948-391A-17	10 US-09-948-391A-19		10 US-09-961-400-24	13 US-10-016-447-2	12 US-10-016-248-89	15 US-10-074-978A-139	13 US-10-016-447-5	12 US-10-037-417-103	9 US-09-981-286A-8	12 US-10-461-713-50	12 US-10-461-713-57	9 US-09-286-240-6
105	104	104	83	83	111	111	117	117	111	110	110	110	111	111	111	110	110	110	169	119	119	124	124	124	124	119	147
95.2	92.1	91.6	74.0	74.0	48.2	48.2	48.2	48.2	48.0	47.3	47.2	47.2	47.2	47.2	47.0	46.3	46.3	46.3	26.5	24.3	24.3	21.1	20.0	18.7	18.7	18.1	17.8
556 548	538 538	535	432	432	281.5	281.5	281.5	281.5	280.5	276.5	275.5	275.5	275.5	275.5	274.5	270.5	270.5	270.5	154.5	142	142	123.5	117	109	109	105.5	104
16	13 13	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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Sequence 8, Application US/09961400
; Beduence B, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
    APPLICANT: RYBAK, SUSANNA M.
    APPLICANT: RYBAK, SUSANNA M.
    APPLICANT: GOLDENBERG, DAVID M.
    TITLE OF INVENTION: LEALIS
    FILE REPRENCE: 01873/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR FILING DATE: 2000-09-25
; PRIOR FILING DATE: 1999-03-26
; PRIOR FILING DATE: 1999-03-26
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PATCHTIN Ver. 2.1
; SEQ ID NO 8
: LEMGHT: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 584; DB 10; Best Local Similarity 100.0%; Pred. No. 3.1e-60; Matches 105; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Rana pipiens
US-09-961-400-8
RESULT 1
US-09-961-400-8
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Query Match
Best Local Similarity 99.0
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: RYBAK, SUGANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-26
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98.5%; Score 575; DB 10; Length 104;
Best Local Similarity 99.0%; Pred. No. 3.5e-59;
Matches 103; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 FEFYLSDCNVISRPCKYKLKKSTNIFCVICENQAPVHFVGVGHC 104
                                                                                                                                 APPLICANT: Newton, Dianne M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: 05200-14110 UNS
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015200-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT PILING DATE: 1998-03-21
PRIOR PILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
SOFTWARE: Patentin Ver. 2.0
                                                                Sequence 4, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09961400 Publication No. US20030124131A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 104
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; ORGANISM: Rana pipiens
US-09-961-400-4
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LENGTH: 104
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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNCCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT TITLE OF INVENTION: CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 MQDWLTPQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPBFVKAICKGIIASKNVLT
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         Length 104;
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                                                                                                                                                                                                                                 62 FEFYLSDCNAISRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                     61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                               1; Indels
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APPLICANT: Newton, Dianne I.
APPLICANT: The United States of America
APPLICANT: Sergresented by The Secretary of the
APPLICANT: Sergresented by The Services
ITILE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
   Score 575; DB 10;
Pred. No. 3.5e-59;
0; Mismatches 1;
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Pred. No. 8.4e-59;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR PLILING DATE: 2000-08-17
PRIOR PLILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR PLILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 9, Application US/09961400; Publication No. US20030124131A1; GENERAL INFORMATION:
98.5%;
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98.1%;
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                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens OTHER INFORMATION: ribonuclease with Met at position 1 and Met24Leu OTHER INFORMATION: substitution (recombinant Met(-1) RaPLR1 Met23Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens OTHER INFORMATION: ribonuclease with (His)6 tag, Met at position 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION: ribonuclease with (His)6 tag, Met at position INFORMATION: and Met30Leu substitution (recombinant Met(-1) INFORMATION: RaPLR1 Met23Leu-(His)6)
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0
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Pred. No. 1.1e-58;
0; Mismatches 2; Indels
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APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REPERENCE: 015280-343110US
CURRENT APPLICANION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR APPLICATION NUMBER: WS 09/622,613
PRIOR PPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver: 2.0
LENGTH: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
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98.1%;
                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 98.1<sup>3</sup>
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Simi
Matches 103;
                                                                                                                                                                                                                                                                                                          US-09-948-391A-8
                                                                                 SEQ ID NO 8
LENGTH: 105
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RESULT 7

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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TAPLICANT: GOLDENBERG, DAVID M.
TILLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TILLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MQDWLTFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKALCKGIIASKNVLT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: Description of Artificial Sequence:Rana pipiens; OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant; CTHER INFORMATION: Met(-1) RapLR1)
US-09-948-391A-6
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                                                                             APPLICANT: Newton, Dianne N.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REPERENCE: 015280-3431100S
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: W0 PCT/US99/06641
PRIOR FILING DATE: 1999-03-27
PRIOR PELICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARR: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 97.6%; Score 570; DB 10; al Similarity 97.1%; Pred. No. 1.3e-58; 102; Conservative 1; Mismatches 2;
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Pred. No. 1.3e-58;
Sequence 6, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09961400 Publication No. US20030124131A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Rana pipiens
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Best Local Similarity
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Best Local 9
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1 MSDWLTFQKKHITUTRDVDCNVIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT FITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-17
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
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                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens OTHER INFORMATION: ribonuclease with Met at position 1 and Gln2Ser OTHER INFORMATION: substitution (recombinant Met(-1) RapLR1 Q1S)
                                                                                                                                                                                                                                                    Length 105;
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The United States of America
as represented by The Secretary of the
Department of Health and Ruman Services
                                                                                                                                                                                                                                                    Score 565; DB 10;
Pred. No. 5.1e-58;
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Pred. No. 5.1e-58;
1; Mismatches 3;
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Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: APPLICANT: as represented by The Secret
APPLICANT: Department of Health and Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/09961400 Publication No. US/03030124131A1 GENERAL INFORMATION: APPLICANT: RYBAK, SUSANNA M.
                                                                                                                                                                                                                                                 96.78;
                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 96.2'
Matches 101; Conservative
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SEQ ID NO 13
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; ORGANISM: Rana pipiens
US-09-961-400-13
                                                                                                                                                                                                                                                                              Best Local Similarity
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US-09-948-391A-28
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US-09-961-400-13
     SEQ ID NO 13
LENGTH: 105
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                                                                                                        FEATURE:
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Publication No. US20030124131A1

GENERAL INFORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: METON DIANNE L.

ITILE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT PILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 09/622,613

PRIOR APPLICATION NUMBER: PCT/US99/06641

PRIOR PILING DATE: 1999-03-26

PRIOR APPLICATION NUMBER: PCT/US99/06641
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     Gaps
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                                                                                                                                                                              61 TFEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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     Indels
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Sequence 13, Application US/09948391A

Sequence 13, Application US/09948391A

Publication No. US20030027311A1

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.

APPLICANT: The United States of America

APPLICANT: The United States of America

APPLICANT: as represented by The Secretary of the

APPLICANT: Department of Health and Human Services

ITILE OF INVENTION: Recombinant Anti-Tumor RNase

FILE REFERENCE: 015280-343110US

CURRENT FILING DATE: 2002-05-10

PRIOR APPLICATION NUMBER: US 60/079,751

PRIOR APPLICATION NUMBER: WO PCT/US99/06641

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1090-03-1

PRIOR FILING DATE: 1090-03-1
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Pred. No. 5.1e-58;
1; Mismatches 2;
  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 96.7%;
Best Local Similarity 97.1%;
Matches 101; Conservative
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102; Conservative
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US-09-961-400-2
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US-09-961-400-2
Matches
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US-09-961-400-11
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: RYBAK, DAVID M.

APPLICANT: NEWTON, DIANNE L.

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

FILE REFERENCE: 018733/1059

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT APPLICATION NUMBER: 09/622,613

PRIOR FILING DATE: 2000-08-17

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VET: 2.1

SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Rana pipiens ribonuclease (RaPLR1) Clone 5alb cDNA; OTHER INFORMATION: insert US-09-948-391A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 6.4e-58;
1; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCBNQAPVHFVGVGHC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.7%; Score 565; DB 10; 97.1%; Pred. No. 6.4e-58;
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
                                              PRIOR APPLICATION NUMBER: US 60/079/948,391A
PRIOR PILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-26
PRIOR PLILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR PLILING DATE: 1999-03-26
PRIOR PLILING DATE: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 96.7%;
Best Local Similarity 97.1%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                       LENGTH:
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APPLICANT: SYBAN, AND AND APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONUUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 01873/1059
CURRENT APPLICATION NUMBER: 09/622,613
FRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR RILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PARENTIN OF SEQ ID NOS: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 DWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens; OTHER INFORMATION: ribonuclease with GlniSer substitution; CTHER INFORMATION: (recombinant RaPLR1 Q1S)
US-09-948-391A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 EFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 BFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                        APPLICANT: Nyacton, Dianne H.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of the Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-34311008
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR PILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR PILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1098-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR PRIOR DATE: 1098-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIN Ver. 2.0
Sequence 11, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 11, Application US/09961400; Publication No. US20030124131A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                       APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 97.1
Matches 100; Conservative
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ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-961-400-11
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; 0

 Query Match
 95.9%;
 Score 560;
 DB 10;
 Length 104;

 Best Local Similarity
 97.1%;
 Pred. No. 1.9e-57;
 atches 100;
 Conservative
 1;
 Mismatches
 2;
 Indels
 0;
 Gaps
 0;

 Qy
 3 DWLFPQKKHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTF
 62

 DD
 2 DWLTFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
 61

Search completed: May 7, 2004, 21:51:56 Job time : 33.6904 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 7, 2004, 21:38:36 ; Search time 9.5276 Seconds (without alignments) 1060.090 Million cell updates/sec Run on:

US-09-961-400-8 Title: Perfect score:

1 MQDWLTFQXKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 584 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		<b>%</b>			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	QI	Description
	540	92.5	104	N	A39035	ribonuclease-relat
7	283.5	48.5	111	-4	JX0120	ribonuclease-relat
e	283	48.5	111	7	A27121	ribonuclease-relat
4	259.5	44.4	111	7	JX0085	pancreatic ribonuc
5	142	24.3	119	~	S41111	pancreatic ribonuc
9	123	21.1	125	Н	A32474	
7	119	20.4	124	Н	NRUI	
æ	117	20.0	124	ч	NRWHK	
თ	114	19.5	128	Н	NRGPB	pancreatic ribonuc
10	113.5	φ.	145	-	A35932	
11	113	19.3	128	Н	NRCU	pancreatic ribonuc
12	111	19.0	125	-	B43825	angiogenin - rabbi
13	109.5	18.8	147	~	152489	
14	109	18.7	124	Н	NRBOB	pancreatic ribonuc
15	109	18.7	128	Н	NRKS	
16	109	18.7	150	П	NRBO	pancreatic ribonuc
17	108	18.5	124	71	S08549	
18	107.5	18.4	123	Н	A43825	angiogenin - pig
19	106	18.2	124	Н	NRSH	
20	106	18.2	124	-1	NRPRH	
21	106	18.2	124	Н	NRHP	
22	106	18.2	124	٦	NRCB	pancreatic ribonuc
23	106	18.2	124	7	S07141	pancreatic ribonuc
24	106	18.2	128	Н	NRYY	pancreatic ribonuc
25	105	18.0	124	Н	NRWB	
56	105	18.0	124	Н	NRGN	pancreatic ribonuc
27	104	17.8	124	٦	NRGF	
28	104	17.8	124	П	NRPG	
29	104	17.8	147	П	NRHUAG	angiogenin precurs

pancreatic-type ri	pancreatic ribonuc	eosinophil-associa	pancreatic ribonuc												
S20066	NRDEO	NRCM	NRCMM	NRCMB	NRHO	S08546	NRGT	NRHY	NRPQ	NRANE	NREKN	NRGPA	JX0115	JC6159	NRANT
7	Н	Н	۲-4	Н	Н	~	Н	н	н	Н	Н	Н	N	~	Н
167	124	124	124	124	128	124	124	124	128	124	124	124	119	155	124
17.8	17.3	17.1	17.1	17.1	17.1	17.0	17.0	17.0	17.0	16.8	16.8	16.8	16.7	16.7	16.6
	101 17.3									98 16.8		98 16.8		97.5 16.7	

## ALIGNMENTS

RESULT 1 A39035 ribonuclease-related anti-tumor protein - northern leopard frog (fragment) C;Species: Rana pipiens (northern leopard frog) C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993 C;Accession: A39035; R;Arcelet, W.; Mikulski, S.M.; Shogen, K. J. Biol. Chem. 266, 245-251, 1991 A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl A;Reference number: A39035; MUID:91093131; PMID:1985896 A;Recession: A39035 A;Retus: preliminary A,Nolecule type: protein A;Residues: 1.104 <ard> C;Superfamily: pancreatic ribonuclease</ard>	and earl
Query Match 92.5%; Score 540; DB 2; Length 104;  Best Local Similarity 92.3%; Pred. No. 2.88-47;  Matches 96; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  QV 2 QDWLFPQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61	
Oy 62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105	
RESULT 2 UX0120	

Cibecies: Rana japonica (Japanese frog)
Cispecies: Rana japonica (Japanese frog)
Cispecies: Rana japonica (Japanese frog)
Cispecies: Rana japonica (Japanese frog)
Cipate: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999
Cipate: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999
Rikamiya, Yi; Oyama, Fi; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi, J. Biochem. 108, 139-143, 1990
A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A;Reference number: JX0120; MUID:91035319; PMID:2229005
A;Accession: JX0120
A;Molcaule type: protein
A;Esidues: 1-111 < KAM
A;

Gaps 7, Query Match 48.5%; Score 283.5; DB 1; Length 111; Best Local Similarity 45.9%; Pred. No. 1.7e-21; Matches 51; Conservative 21; Mismatches 32; Indels 7;

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A Contents: annotation; conformation by (1)H-NMR, residues 1-125
Ricquin, 0.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
Ricquin, 0.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
A;Title: Solution structure of bovine angiogenin by (1)H nuclear magnetic resonance sh; Reference number: A58821; MUID:96280645; PMID:8688423
A;Contents: annotation, conformation by (1)H-NMR
R;Relsdorf, C.; Abergel, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, Eur. J. Blochem. 224, 811-822, 1994
      C;Species: Iguana iguana (common iguana)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: 841111
R;Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Bir. J. Biochem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A;Reference number: 841111; MJID:94139745; PMID:8307028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Proton resonance assignments and secondary structure of bovine angiogenin. A;Reference number: S48212; MUID:95010071; PMID:7925406
A;Contents: annotation; conformation by (1)H-NWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Argerimmental source: milk
RiAcharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
Submitted to the Brookhaven Protein Data Bank, January 1995
A;Reference number: A65065; PDB:1AGI
A;Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125
RiAcharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
RiAcharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
RiAcharya, A.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
A;Reference number: A58315; MUID:95224057; PMID:7708754
A;Contents: annotation; X-ray crystallography, 1.5 angstroms
R;Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
Submitted to the Brookhaven Protein Data Bank, April 1996
A;Reference number: A65709; PDB:1GIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-Sep-1989 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QDWLTFQKKHL-----TNTRDVDCNNIL---STNLFHCKDKNTFIYSRPEPVKAIC--K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G.; Tartar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 GIIASKNVLTTFE-FYLSDC----NATSRPCKYKLKKSTNTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Maes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartax
FBBS Lett. 241, 41-45, 1988
A;Title: The complete amino acid sequence of bovine milk angiogenin.
A;Reference number: S02001; MUID:89065101; PMID:3197838
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Bond, M.D.; Strydom, D.J.
Biochemistry 28, 6110-6113, 1989
A;Title: Amino acid sequence of bovine angiogenin.
A;Reference number: A32474; MUID:89375344; PMID:2775757
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                  24.3%; Score 142; DB 2; 29.8%; Pred. No. 3e-07; iive 19; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Bos primigenius taurus (cattle)
C;Date: 25-Sep-1989 #sequence revision 25-Se
C;Accession: A32474; S02001; A30044; S48212
                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N, Alternate names: angiogenesis factor N, Contains: ribonuclease (EC 3.1.27.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      angiogenin [validated] - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: protein
A,Residues: 1-125 <BON>
A,Experimental source: plasma
                                                                                                                                                                                                                                      A, Accession: S41111
A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-119 <ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: S02001
A,Molecule type: protein
A,Residues: 1-125 <MAE>
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A32474
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C;Species: Rana catesbeiana (bullfrog)
C;Species: Rana catesbeiana (bullfrog)
C;Bate: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: JX0085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
J; Biochem. 106, 729-735, 1989
A;Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A;Reference number: JX0085; MUID:90130374; PMID:2613682
A;Accession: JX0085
A;Accession: JX0085
A;Accession: JX0085
A;Accession: JX0085
A;Residues: 1-111 <ANTP-
C;Superfamily: pancreatic ribonuclease
C;Keywords: hydrolase; pyroglutamic acid (Gln) #status experimental
F;10,35,104/Active site: Pyrollidone carboxylic acid (Gln) #status predicted
F;10,35,104/Active site: His, Lys, His #status predicted
F;10-72,34-82,52-97,94-111/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                              ribonuclease-related sialic acid-binding lectin - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Species: Rana catesbeiana (bullfrog)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C;Accession: A27121
B;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanagi
B;Cchemistry 26, 2189-2194, 1987
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A;Reference number: A27121; MUD:87299649; PMID:3304421
A;Reference number: Drotein
A;Residues: 1-111 -TIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5,
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QDWLTFQKKHLINTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                    2 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                           58 VLTIFEFYLSDC--NATS-RPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                58 VLTTFEFYLSDCNATS---RPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 VLTTFEFYLSDC---NATSRPCKYKLKKSTNTFCYTCENQAPVHFYGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
&
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.4%; Score 259.5; DB 2;
42.3%; Pred. No. 4.4e-19;
iive 18; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.5%; Score 283; DB 2;
48.6%; Pred. No. 1.9e-21;
ive 15; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
841111
pancreatic ribonuclease - common iguana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
ses 47; Conserv
                                                                                                                                                                                           61
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R; van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J Bur. J. Biochem. 75, 91-1100, 137.
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a A;Reference number: A91247; MUID:77185023; PMID:862624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues C; Superfamily: pancreatic ribonuclease C; Keywords: and logenesis; hydrolase: micleic ciril documents by hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: pancreatic ribonuclease; Superfamily: pancreatic reid degradation; pyroglutamic acid; Keywords: angiogenesis; hydrolase; nucleic acid
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 LTFQKKHL-----TNTRDVDCNNIL---STNLFHCKDKNTFIYSRPEPVKAIC--KGII 53
                                                                                                                                                                                                                                                                                                                                                                                                                                    62 NVLCKNGRINCYESNSIMHITDCRQIGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C;Accession: A35932
B;Cohem. Biophys. Res. Commun. 171, 988-995, 1990
A;Title: Isolation and sequencing of mouse angiogenin DNA.
A;Reference number: A35932
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-145 < BON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LTFQKKHLTNTRDVD-----CNNILSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK
                                                                                                                                                                                                                                                                                                    6 MKFOROHMDSGNSPGNNPNYCNOMMRRKMTQGRCKPVNTFVHESLEDVKAVC----SOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 CKNGQINCYQSYSRMRIIDCRVISSSKFPNCSYRMSQAQKSIIVACEGDPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                      -TTFEFYLSDCNATSRP----CKYKLKKSTNTFCVTCENQ--APVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 ASKNVLTTFEFY----LSDCNATSRP----CKYKLKKSTNTFCVTCENQ--APVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A00826
A;Molecule type: protein
A;Residues: 1-128 <VAN.
A;Note: 64-Pro Was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      guinea pig (tentative sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326 C, Genetics:
A,Intros: #status absent
C,Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                     28;
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                                                                                                   Length 124;
                                                                                                ; Score 117; DB 1; Length 12.; Pred. No. 0.0001; 16; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.5%; Score 114; DB 1;
25.0%; Pred. No. 0.00021;
tive 25; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pancreatic ribonuclease (EC 3.1.27.5) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Alternate names: angiogenesis factor N; Contains: ribonuclease (EC 3.1.27.-)
                                                                                                       20.0%;
26.9%;
                                                                                                   Query Match 20.0
Best Local Similarity 26.9
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiogenin precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N; Alternate names: RNase IB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         57 NVL----
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J. Mol. Evol. 19, 145-152, 1983
A;Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the ami
A;Reference number: A92957; MUID:87036770; PMID:6571219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pancreatic ribonuclease (EC 3.1.27.5) - minke whale
NiAlternate names: RNase 1, RNase A
C;Species Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A00818
R;Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A;Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A;Reference number: A00818; MUID:76277855; PMID:962870
                                         A; Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 1-124 * DBI>
A;Note: about one-third of the molecules lacked Ala-1
C;Comment: The cuis is a rodent belonging to the same subfamily as the guinea pig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pancreatic ribonuclease (EC 3.1.27.5) - cuis
N'Alternate names: RNase 1; RNase A
C;Species: Galea musteloides (cuis)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 04-Oct-1996
C;Accession: A00827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCKNGQTNCYQSHSSMRITDCRVTSSSKYPNCSYRMTQAQKSIIVACEGTPSVPUHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                       24 DEYCFUMMKURRLTRPCKDRNTFIHGNKNDIKAICEDRNGQPYRGDLRISKS----EFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 MKFOROHMDSDGHPDTNTN--YCNEMMVRRSMTQGRCKPVNTFVHEPLEAVQAVCSQKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LIFQKKHL-----INTRDVDCNNIL---SINLFHCKDKNTFIYSRPEPVKAIC--KGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 IASKNVLTTFEFY----LSDCNATSRP----CKYKLKKSTNTFCVTCEN--QAPVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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A,Molecule type: protein
A,Roledues: 1-124 <EMM>
C,Superfamily: pancremts
C,Superfamily: parceric ribonuclease
C,Keywords: glycoprotein, hydrolase, nucleic acid digestion, pancreas
F,12,41,119/Active site: His, Lys, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: pancreatic ribonuclease
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119,40-totive site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72Disuifide bonds: #status predicted
F;94/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
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                                                                                                                                                                                                                                                                         Length 125;
                                                                                                                                                                                                                                                                     21.1%; Score 123; DB 1; Length 12 ilarity 32.7%; Pred. No. 2.5e-05; Conservative 14; Mismatches 32; Indels
                                                                    C;Superfamily: pancreatic ribonuclease
C;Keywords: angiogenesis; hydrolase; nucleic acid degradation
                                                                                                                                  F;60_68/Region: receptor binding #status predicted F;14,41,115/Active site: His, Lys, His #status predicted F;27-82,40-93,58-108/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 LSDC---NATSR-PCKYKLKKSTNTFCVTCENQAPVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                     17 DVDCNNILSTNLF--HCKDKNTFIYSRPEPVKAICK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A00827
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Gaps

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Gaps

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pancreatic ribonuclease (BC 3.1.27.5) - American bison (tentative sequence) NyAlternate names: RNase 1; RNase A C; Species: Bison bison (American bison and C; Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 08-Dec-1994 C; Accession: A91771; A90270; A94696; A00804
               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GDB:6108046; OMIM:601030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: 14q24-q31
A,Introns: #status absent
C,Superfamily: pancreatic ribonuclease
               13;
                                                               CKDKNTF1YSRPEPVKAICK-
                                                                                                                                                                                                        99 GSRNIVIACENGLPVHF 115
                                                                                                                                                               66
                                                                                                                                                          83 STNTFCVTCENQAPVHF
               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein A; Residues: 29-147 <ZHO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S60163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S38272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB:RNASE4
               23;
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               Matches
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NRBOB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: A00822
B; van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A; Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic A; Reference number: A90612; MUID:77065676; PMID:999896
A; Reference number: A90612; MUID:77065676; PMID:999896
A; Residues: 1-128 «VAN»
C; Superfamily: pancreatic ribonuclease
C; Superfamily: pancreatic ribonuclease
C; Reywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F; 24, 41.119/Active site: His, Lys, His #status predicted
F; 26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
F; 34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                     mature form) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Species: Myocastor coypus (nutria, coypu)
| Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LCKNGQTNCYQSNSNWHHTTDCRVTSNSDYPNCSYRTSQBEKSIVVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Species: Oryctolagus cuniculus (domestic rabbit)
;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
;Accession: S29833; B43825
                                                                                                                                                                                                                                                   CKDKNTFIYSRPEPVKAIC--KGIIASKNV-LTTFEFYLSDCNATS----RPCKYKLKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TIFEFYLSDCNATSRP----CKYKLKKSINTFCVICENQ--APVHF 99
                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Oryccolagus cuniculus (domestic rabbit)
C;Species: Oryccolagus cuniculus (domestic rabbit)
C;Daccession: S2983; H81825
R;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse anginatelescence number: 829833; MUID:93192291; PMID:8448182
A;Acterior number: 829833; MUID:93192291; PMID:8448182
A;Actus: prelliminary
A;Molecule type: protein
A;Residues: 1-125 <BON>
A;Note: submitted to the Protein Sequence Database, December 1992
C;Superfamily: pancreatic ribonuclease
C;Seywords: pyrcglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimen
                                                                                                                                                                                                          7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - nutria (tentative sequence)
                                                                                                                                                        DB 1; Length 145;
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                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Indels
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-145/Product: angiogenin #status predicted <NAT>
F;25/Modifled site: pyrrolidone carboxylic acid (Gln) (in:
F;37.64,137/Active site: His, Lys, His #status predicted
F;50-104,63-115,81-130/Disulfide bonds: #status predicted
                                                                                                                                                                                                        32;
                                                                                                                                                Query Match 19.4%; Score 113.5; DB 1 Best Local Similarity 34.2%; Pred. No. 0.00026; Matches 26; Conservative 11; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.3%; Score 113; DB 1; 27.4%; Pred. No. 0.00026; iive 19; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 111; DB 1;
Pred. No. 0.00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pancreatic ribonuclease (EC 3.1.27.5)
N;Alternate names: RNase 1; RNase A
                                                                                                                                                                                                                                                                                                                                                                                            123 FRHVVIACENGLPVHF 138
                                                                                                                                                                                                                                                                                                                                                 84 INTECVICENQAPVHF 99
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29.9%;
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Best Local Similarity
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Matches 32; Conserv
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chromosomal localization and i
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                                                                                                                                                                                                                                                                                                                                                                           ribonuclease 4 (EC 3.1.-.-) precursor - human
N;Alternate names: RNase 4
C;Species: Homo sapiens (man)
C;Date: 02-Jul.1996 #sequence revision 02-Jul-1996 #text_change 22-Jun-1999
C;Accession: I52489; S60163; S38272
R;Seno, M; Futami, J; Futshima, Y; Akutagawa, K; Kosaka, M; Tada, H.; Yamada, I
Biochim. Biophys. Acta 1261, 424-426, 1995
A;Title: Molecular cloning and expression of human ribonuclease 4 cDNA.
A;Reference number: I52489; MUID:95260866; PMID:7742370
   ---RPCKYKLKK 82
                                            FQKKHL----INTRDVDCNNIL---SINLFHCKDKNIFIYSRPEPVKAICK--GIIASKN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 29-53,'D',55-147 <ROS>
A;Cross-references: EMBL:U36775; NID:g1040977; PIDN:AAA96750.1; PID:g1040978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-147 <RES>
A;Cross-references: GB:D37931; NID:g976228; PIDN:BAA07150.1; PID:g976229
R;Rosenberg, H:F; Dyer, K.D.
Nucleic Acids Res. 2, 4290-4295, 1995
A;Title: Human ribonuclease 4 (RNase 4): coding sequence, chromosomal loc A;Reference number: S60163; MUID:96091174; PMID:7501448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 147;
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F;53-109,67-120,85-135,92-99/Disulfide bonds: #status predicted
-GIIASKNV-LTTFEFYLSDCNATS-
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Bicohem. 217, 401-410, 1931

A;Title: The amino acid sequence of human ribonuclease 4, A;Reference number: S38272; MUID:94039064; PMID:8225579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: 152489
A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA
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7, 2004, 21:54:54

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Search completed: May 7
Job time : 10.5276 secs
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R;Beintema, J.J.; Knol, G.; Martena, B.
Biochim. Biophys. Acta 705, 102-110, 1982
A;Title: The primary structures of pancreatic ribonucleases from African porcupine and A;Reference number: A90644; MUID:83000399; PMID:7115727
                                                                                                                                A;Molecule type: protein
A;Residues: 1-124 <MUS>
A;Note: comparison of peptide compositions and partial sequence determination revealed
                                                                                                                                                                                                                             Ristewart, G.R.; Stevenson, K.J.
Blochem. J. 135, 427-441, 1973
Blochem. J. 135, 427-441, 1973
A;Tille: The isolation and partial characterization of ribonuclease A from Bison bison.
A;Reference number: A90270; MUID:74081066; PMID:4772270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: protein
A,Residues: 1-128 <BEI>
A,Note: residues 67-78 were positioned primarily by homology with other ribonucleases
                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: protein
A, Residues: 1-60,62-124 <STE>
A, Residues: 1-60,62-124 <STE>
R, Note: peptide compositions were compared with the bovine sequence
R, Barnard, E.A.; Cohen, M.S.; Gold, M.H.; Kim, J.K.
Nature 240, 395-398, 1972
A, Title: Evolution of ribonuclease in relation to polypeptide folding mechanisms.
A, Reference number: A94696; MUID: 73045781; PMID: 4564316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 PCKNGQSNCYESTSNMHITDCRLTSNSKFPDCLYRTSQEEKSIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Proechimys guairae (casiragua)
C;Date: 17-Mar-1987 #seguence_revision 17-Mar-1987 #text_change 30-Sep-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LITFEFYLSDCNATSR----PCKYKLKKSTNTFCVTCENQ--APVHF 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 NVLTTFEFY----LSDCNATSRP----CKYKLKKSINTFCVTCENQ--APVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: protein
A;Residues: 1-15, E',17,'E',19-20,'XTA',24-30 <BAR>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: pancreatic ribonuclease
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lis, His #status predicted
F;26.84,40.95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Indels
R;Muskiet, F.A.J.; Welling, G.W.; Beintema, J.J.
Int. J. Pept. Protein Res. 8, 345-348, 1976
A;Reference number: A91771; MUID:76259396; PMID:955781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.7%; Score 109; DB 1; 26.5%; Pred. No. 0.00064; tive 19; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pancreatic ribonuclease (EC 3.1.27.5) - casiragua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 28.2'
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.7
Best Local Similarity 26.5
Matches 30; Conservative
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                                                                                                A; Accession: A91771
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US-09-961-400-8 584 1 MQDWLJFQKKHLINTRDVDC.....TFCVTCENQAPVHFVGVGHC 105

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 Total number of hits satisfying chosen parameters:

141681 segs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description		rana	P18839 rana japoni		P80287 iguana igua		Q8wn66 cercopithec					σ.								Q8wn65 miopithecus	soq	Bum	P31346 sus scrofa	P80929 bos taurus				P00672 hippopotamu		P00677 hydrochoeru	_	560 connocha	P07848 gazella tho
ID	RN30 RANPI	RNPO RANCA	LECS RANJA	RNPL RANCA	RNP IGUIG	ANGE MOUSE	ANGI CERAE	ANGI_BOVIN	RNP GALMU	RNP BALAC		RNPB CAVPO	ANGI MOUSE	RNP MYOCO	ANGI PAPHA	RNS4 PANTR	ANGI_RABIT	RNS4 HUMAN	RNP PROGU	ANGI MIOTA	RNP BOVIN	ECP4 MOUSE	ANGI PIG	ANG2 BOVIN	RNP AEPME	RNP ANTAM	RNP CHIBR	RNP HIPAM	RNP_SHEEP	RNP HYDHY	RNP_BUBBU	RNP CONTA	RNP GAZTH
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Q8wn62 saguinus oe	P00662 giraffa cam	P00671 sus scrofa	Q8wn60 saimiri sci	P03950 homo sapien	Q8wme8 pan troglod	P39873 bos taurus	P15467 bos taurus	035290 mus musculu	Q9wusl myoxus glis	046529 saimiri sci	Q29542 giraffa cam
ANGI_SAGOE	RNP GIRCA	RNP_PIG	ANGI SAISC	ANGI HUMAN	ANGI PANTR	RNBR_BOVIN	RNS4 BOVIN	ECP3 MOUSE	RNP MYOGL	RNS6 SAISC	RNBR_GIRCA
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18.0	17.8	17.8	17.8	17.8	17.8	17.8	17.7	17.6	17.6	17.6	17.5
105	104	104	104	104	104	104	103.5	103	103	102.5	102
34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                            ABJURE 98437383; PubMed=9761686; Chang C.-F., Huang T.H.; Chang C.-F., Chen C., Chen Y.-C., Hom K., Euang R.-F., Huang T.H.; The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbelana (bullifog) "; J. Mol. Biol. 283:231-244(1998)"; FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine -: FUNCTION: Preferentially cleaves
                                                                                                                                                                                residues with a 3'flanking guanne. Hydrolyzes poly(0) and poly(0) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin aggluthates various animal cells, including hormal lymphocytes, erythrocytes, and fibroblasts of animal and buman origin. It is cytotoxic against several tumor cells.
                TISSUE=Egg;
MEDLINE=93192604; PubMed=8448385;
Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
Takayanagi Y., Hakomori S., Titani K.;
"Ribonuclease activity of sialic acid-binding lectin from Rana
                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF039104; AAD10702.1; -.
                                                                      catesbeiana eggs.";
Glycobiology 3:37-45(1993)
                                                                                                       STRUCTURE BY NMR OF 23-133.
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Matches 55; Conserv
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MEDLINE-98165825; PubMed=9497370;
Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
Huang Hana catesbeina ror gene encoding a cytotoxic ribonuclease.
Tissue distribution, cloning, purification, cytotoxicity, and active
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H., Takayanagi G., Hakomori S.;
"Amino acid sequence of sialic acid binding lectin from frog (Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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"A pyrimidine-guanine sequence-specific ribonuclease from Rana
                                                                                                                                                                                                                          Length 104;
                                                                                                                                                                                                                                                                                                          62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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                                                                                                                                                                                                  11845 MW; 22A753C2F9E566B4 CRC64;
                                                                                                                                                                                                                     93.0%; Score 543; DB 1;
93.3%; Pred. No. 1.4e-51;
ive 3; Mismatches 4;
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CHARACTERIZATION, AND SEQUENCE OF 81-101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catesbeiana (bullfrog) oocytes.";
Nucleic Acids Res. 20:1371-1377(1992).
[4]
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J. Biol. Chem. 273:6395-6401(1998)
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MEDLINE=87299649; PubMed=3304421;
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                                                                                                                                                                                                                                             Conservative
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PIR; A27121; A27121.
PDB; 1BC4; 28-0CT-98.
PDB; 1MO7; 21-JAN-03.
InterPro; 1PR001427; RNaseA.
Prodom, P0000535; RNaseA; 1.
Prodom; P0000535; RNaseA; 1.
PROSITE; P800127; RNASE P5, 1.
PROSITE; P800127; RNASE P5, 1.
PROSITE; P800127; RNASE PANCREATIC; 1.
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49.5%; Pred. No. 6.9e-24;
iive 14; Mismatches 34;
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2 QDWLIFQKKHLINIRDVDCNNILSINLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
NCBI TaxID=8517;
                                                                                                           kana catespelana (bull Irog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biochem. 106:729-735(1989).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphotligonucleotides ending in C-P or with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Descreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D64BA72456C10788 CRC64;
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44.4%; Score 259.5; DB 1;
Best Local Similarity 42.3%; Pred. No. 4e-21;
Matches 47; Conservative 18; Mismatches 39;
01-APR-1990 (Rel. 14, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Libonuclease, liver (EC 3.1.27.5).
Rana catesbeiana (Bull frog).
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PROSITE; PS00127; RNASE PANCREATIC; 1.
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                                                                                                                                                                                                                                                                                   MEDLINE=90130374; PubMed=2613682;
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HSSP; P11916; 1BC4.
InterPro; IPR001427; RNaseA.
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ProDom; PD000535; RNaseA; 1.
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P80287;
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RNP_IGUIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
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          57
                                             QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. 108:139-143(1990).

- FUNCTION: The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin preferentially agglutinate a large variety of tumor cells, but it does not agglutinate non-transformed cells and erythrocytes.

- SUBUNIT: Monomer.
          QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
Takayanagi Y., Titani K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLTTFEFYLSDC--NATS-RPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLSTTRFQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1'
                                                                                                                                                              VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR; JX0120; JX0120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 111;
                                                                                                             --RPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00074; rnase4; 1.
Prodom; PD000535; RNaseA; 1.
SMART; SM00092; RNASE P5: 1.
PROSTIE; PS00127; RNASE PANCEATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1111
12326 MW; FDEBDDF3834ED679 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
NCBI_TaxID=8402;
                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (Rel. 16, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
13-10-10-2003 (Rel. 42, Last annotation update)
Rana japonica (Japanese reddish frog).
                                                                                                                                                                                                                                                                                              111 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P11916; 1BC4.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid.
                                                                                                                   58 VLTTFEFYLSDCNATS-
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P14626;
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MOD RES

Best Loca Matches

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7; Gaps

Indels

Length 111;

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Eur. J. Biochem. 219:641-646(1994)

RNPL\_RANCA

RESULT 4

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                                                                                                                                                                                                                                                                                                                                                        QDWLTFQKKHL-----TNTRDVDCNNIL---STNLFHCKDKNTFIYSRPEPVKAIC--K 50
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=129; TISSUE=Liver;
STRAIN=129; TISSUE=Liver;
STRAIN=26079109; PubMed=8530072;
Brown W.E., Nobile V., Subramanian V., Shapiro R.;
"The mouse angiogenin gene family: structures of an angiogenin-related protein gene and two pseudogenes.";
Genomics 29:200-206(1995).
-:- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                      16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        GIIASKNVLTTFE-FYLSDC----NATSRPCKYKLKKSTNTFCVTCENQAPVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphooligonucleotides ending in C-P or with 2',3'-oyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                  45; Indels
                                                                                                                                                 SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic
MOD_RES 1
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                 6072FB5B7B15BD5A CRC64;
                                                                                                                                                                                                                                                                                                                       Pred. No. 1.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ANGRP.
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                                                                                                                                                                                                                                                                                                       24.3%; Score 142;
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                                                                                     HSSP, P00656, 1LSQ.
InterPro, IRR001427; RNaseA.
Pfam, PF00074; rnaseA, 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                 13324 MW;
                                                                                                                                                                                                                                                                                                                   29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:104984; Angrp.
InterPro; IPR001427; RNaseA.
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                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                  91
106
10
40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                119 AA;
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                            SEQUENCE
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Pfam; PF00074; rnaseA; 1.

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MEDLINE-21918422; PubMed=11919285;

A Zhang J., Rosenberg H.F.;

The Triang J., Rosenberg H.F.;

The Triang Selection of the tumor-growth promoter angiogenin in primate evolution.";

Mol. Biol. Evol. 19:438-445(2002).

L. FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (BP similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                            63 CKDVNTFIHDTKNNIKALGGKKGSPYGRNLERISKSRFQVTTCTHKGRSPRPFCRYRASKG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Buropean Bioinformatics Institute. There are no restrictions on its way by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       CKDKNTFIYSRPEPVKAIC--KGIIASKNV-LTTFEFYLSDCNATSR----PCKYKLKKS 83
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                  PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                  21.5%; Score 125.5; DB 1; Length 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                                                                                                                                                                                                                                                                                                                                                                       30; Indels
                                                                                                                                   ANGIOGENIN-RELATED PROTEIN
                                                                                                                                                                                                                                                                                                29A6EB814429C4AD CRC64;
                                                                                                                                                                                                                                                                                                                                                        1.3e-06;
                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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ProDom; PD000535; RNaseA; 1.
SMRRT; SW00092; RNAse Pc; 1.
PROSITE; PS00127; RNASE PAWCREATIC; 1.
Signal; Hydrolase; Nuclease; Endonuclease;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                      36.8%; Pred. No. 1.36 ive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                                                                                                                                  16612 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
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                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                 145
25
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137
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63
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81
145 AA;
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RNP GALMU P00680;
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Matches
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RNP_GALMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                   53 TMRRRHLTSP------CKDINTFIHGNRHHIKAICGDENGNPYGENLRISK 97
                                                                                                                                                                                                                                                                                                                                                                 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-MEAN BENDES 197838; MEDLINE-MEAN BENDES 197838; Maes P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A.; "The complete amino acid sequence of bovine milk angiogenin.";
                                                                                        carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bond M.D., Vallee B.L., \fill \fil
                                                                                                                                                                                                                                                                                                                           DB 1; Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and expression of bovine angiogenin."; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                               31; Indels
                                                                                                                                                                                                                                                                                           27860112E85B8DF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 FEFYLSDCN----ATSRPCKYKLKKSINTFCVTCENQAPVH 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 SPFQVTTCNLRGGSPRPPCOYRATRGSRNIVVGCENGLPVH
                                                                       Hydrolase, Nuclease, Endonuclease, Angiogenesis, Protein synthesis inhibitor, Signal, Pyrrolidone SIGNAL 24 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                         Score 123.5; DB 1
Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Angiogenin-1 precursor (EC 3.1.27.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bond M.D., Strydom D.J.;
"Amino acid sequence of bovine angiogenin.";
                                                                                                                                                            SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                            Pred. No. 2.1e-17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION, AND SEQUENCE OF 25-55.
                                                                                                                                ANGIOGENIN.
                                                      PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89375344; PubMed=277575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89118214; PubMed=3064806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibitor binding assay.";
Biochemistry 27:6282-6287(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 28:6110-6113(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANGI BOVIN STANDARD;
P10152; Q9GKP9;
01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                                                                           16444 MW;
   PRINTS; PR00794; RIBONUCLEASE
                                                                                                                                                                                                                                                                                                                               21.1%;
29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lett. 241:41-45(1988).
                        RNaseA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning, sequencing, and Submitted (MAR-1999) to the
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 29.78
Matches 30, Conservative
                    ProDom; PD000535; RNaseA;
SMART; SM00092; RNASe_PC;
PROSITE; PS00127; RNASE_P
                                                                                                                                                                                                  64
138
105
116
                                                                                                                              146
25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [3]
SEQUENCE OF 24-148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 24-148.
                                                                                                                                                                                                                                                                                           146 AA;
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                                                                                                                              25
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DISULFID
SEQUENCE
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ACT_SITE
ACT_SITE
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MOD_RES
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                                                                                                                                                                                                                17 DVDCNNILSTNLF--HCKDKNTFIYSRPEPVKAICK------GIIASKNVLTTFEFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Gaps
                                                                                                                                                    MEDLINE=96280645; PubMed=8688423;
Lequin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
"Solution structure of bovine angiogenin by 1H nuclear magnetic
             MEDLINE=95224057; PubMed=7708754; Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.; "Crystal structure of bovine angiogenin at 1.5-A resolution."; Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16969 MW; B7999124CBB523DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 ITICKHKGGSSRPPCRYGATEDSRVIVVGCENGLPVHF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 LSDC---NATSR-PCKYKLKKSTNTFCVTCENQAPVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein synthesis inhibitor; Signal; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.1%; Score 123; DB 1;
llarity 32.7%; Pred. No. 2.5e-06;
Conservative 14; Mismatches 32;
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21-JUL-1986 (Rel. 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANGIOGENIN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF135124; AAG47631.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001427; RNaseA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37
64
138
105
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PDB; 1GIO; 07-DEC-96.
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es 32; Conserv
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MACMU
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|- SINILARITY.
|- SINILARITY.
| PIR; A00827; NRUI.
| HSSP; P00555; NSNO.
| InterPro; IPRO01427; RNAS.
| DR PRINTES; PRO0074; INASE_PO.
| DR PRINTES; PRO0052; RNASE_PO.
| DR PROSITE; PRO0127; RNASE_PO.
| PROSITE; PRO0127; RNASE_PORCREATIC; I.
| PROMITER | PROMICARITY.
| SIMILARITY.
| PROMITER | PROMICARITY.
| PROMITER | PROMITER | PROMICARITY.
| PROMITER | PROMITER | PROMICARITY.
| PROMITER | PR
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                                                                                                                                                                                                        comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 IASKNVLTTFEFY----LSDCNATSRP----CKYKLKKSTNTFCVTCEN--QAPVHF 99
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                                                                                                                                                                                                                                                                        3'-
U-P
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Emmens M., Welling G.W., Beintema J.J.;
"The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Galea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Mysticeti,
                                                                                                                                                                                                                                         "MO1. EVOl. 19:145-552(1993).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphate and 3'-phosphotoligonucleotides ending in C-P or with 2'.3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family. PRSSP. P00656; 1SRN.
InterPro; IPRO01427; RNaseA.
                                                                                                                                                                           Beintema J.J., Neuteboom B., "Origin of the duplicated ribonuclease gene in guinea-pig: com of the amino acid sequences with those of two close relatives: capybara and cuis ribonuclease.",
                       (RNase 1) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.-UUL-1986 (Rel. 01, Last sequence update)
10.0CT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).
RNASEL OR RNS!
     Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 AA
 (Rel. 41, Last annotation e pancreatic (EC 3.1.27.5)
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                                                                                                                                                        MEDLINE=87036770; PubMed=6571219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Balaenopteridae; Balaenoptera.
NCBI_TaxID=9767;
                                                     Galea musteloides (Cuis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                       NCBI TaxID=10146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ribonuclease.";
                                    RNASE1 OR RNS1
                    Ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986
10-OCT-2003
                                                                                                                           SEQUENCE.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 NVLCKNGRINCYESNSTWHITDCRQTGSSKYPNCAYKISQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 NVL-----TIFEFYLSDCNATSRP----CKYKLKKSINTFCVTCENQ--APVHF 99
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"Diversifying selection of the tumor-growth promoter angiogenin in primate evolution.";

"Diversifying selection of the tumor-growth promoter angiogenin in primate evolution.";

"Old Biol. Bvol. 19:438-445(2002).

-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endochtal invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity).

-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                           CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphooligonucleotides ending in C-P or with 2',3'-cyclic phosphate intermediates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                        -!- SUBCELLUTAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the pancreatic ribonuclease family.
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28-FBB-2003 (Rel. 41, Last annotation update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
ANG OR RNASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LINKED (GLCNAC. . .) (30%).
F57475459F697E20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Nuclease; Endonuclease; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 1;
8.9e-06;
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N-LINKED (GICNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                HSSP, P00656, ISRN.
InterPro, IPR001427; RNaseA.
Pfam, PF00074; rnaseA, 1.
PRINTS, PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14125 MW;
Biochem. J. 157:317-323(1976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
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26.9%;
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                                                                                                                                                                                                             PIR; A00818; NRWHK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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Matches
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                          6 TPQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAIC---KGIIASKNV-LTT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary structure and glycosidation.";

Eur. J. Biochem. 75:19-100(1977).

-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
-1- SIBCIELIULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Pancreas.
-1- SIMILARITY: Balongs to the pancreatic ribonuclease family.
-1- HSSP; P00656: ISBN.
                                                                                                                                                                                                                                                                                            23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=77185023; PubMed=862624;
van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastra W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
28-FUUL-1986 (Rel. 01, Last sequence update)
28-FBD-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).
Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Gondata; Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria, Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                ProDom; FDUUUDSD, ANDSE PARSEPTIC; 1.
PRORITE; PRO1092; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
24 BY SIMILARITY.
                                                                                                                                                                                                                                                                      19.6%; Score 114.5; DB 1; Length 146; 27.7%; Pred. No. 2e-05; tive 17; Mismatches 33; Indels 23
                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                         E39A89215DB2A2A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                         62 FEFYLSDC----NATSRPCKYKLKKSTNTFCVTCENQAPVH 98
                                                                                                                                                                              SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 128 AA
                                                                                                                                                           ANGIOGENIN.
                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS, PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe_Pc; 1.
                                                                          Pfam, PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                      16301 MW;
                                                                 InterPro; IPR001427; RNaseA.
                                                       EMBL; AF441667; AAL61649.1;
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                         37
64
138
105
116
                                                                                                                                                 24
146
25
                                                                                                                                                                                                                                                      146 AA;
                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Pancreas;
                                                                                                                                                                                          37
64
138
50
63
81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beintema J.J.;
                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                 RNPB CAVPO
P00679:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                    ACT_SITE
ACT_SITE
                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                               98
                                                                                                                                                                                                                                                                            Query Match
Best Local &
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                         ACT SITE
                                                                                                                                                                                                                                             DISULFID
                                                                                               ProDom;
                                                                                                                                                                      MOD_RES
                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                       CAVPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 MKEĞRQHMDPEGSPSNSSNY-CNVMMIRRNMTQGRCKPVNTFVHESLADVQAVCFQKNVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 LIFQKKHL-----TNTRDVDCNNIL---STNLFHCKDKNTFIYSRPEPVKAIC--KGII 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 CKNGQINCYQSYSRMRIIDCRVISSSKFPNCSYRMSQAQKSIIVACEGDPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 ASKNVLTTFEFY----LSDCNATSRP----CKYKLKKSTNTFCVTCENQ--APVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Anglogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                                                                                                                                                                                                                                                                                                                                                                                            Score 114; DB 1; Length 128;
Pred. No. 1.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       40; Indels
                                               BY SIMILARITY.
N-LINKED (GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                      14406 MW; A2F4101A1A33E93B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91025023; PubMed=2222458;
MEDLINE=91025023; Vallee B.L.;
"Isolation and sequencing of mouse anglogenin DNA.";
Biochem. Biophys. Res. Commun. 171:988-995(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci. U.S.A. 99:16899-16903(2002).
                    Endonuclease; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Mismatches
PANCREATIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                  19.5%;
25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                             Hydrolase; Nuclease;
DISULFID 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           roc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                            128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
  PROSITE; PS00127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FVB/N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANGI MOUSE
                                                                                                             DISULFID
DISULFID
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                         DISULFID
                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                    VARIANT
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64 LCKNGQINCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Biol. Evol. 19,438-445(2002).
-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
-!- coatin on the surface of endothelial cells; once bound,
angiogenin is endocytosed and translocated to the nucleus, thereby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 FQKKHL-----TNTRDVDCNNIL-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 L-----TTFEFYLSDCNATSRP----CKYKLKKSINTFCVTCENQ--APVHF 99
                                                                                                                                                                                             van den Berg A., van den Hende-Timmer L., Beintema J.J.;
"Isolation, properties and primary structure of coypu and chinchilla
pancreatic ribonuclease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=11918422; PubMed=11919285;
Zhang J., Rosenberg H.F.;
"Diversifying selection of the tumor-growth promoter angiogenin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                        Mammalia; Butheria; Rodentia; Hystricognathi; Myocastoridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
ANG OR RAMASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 113; DB 1; Length 128; Pred. No. 2.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Hydrollase; Nuclease; Endonuclease; Glycoprotein. |
| Hydrollase; Nuclease; Endonuclease; Glycoprotein. |
| DISULFID 26 84 BY SIMILARITY. |
| DISULFID 40 95 BY SIMILARITY. |
| DISULFID 58 110 BY SIMILARITY. |
| ACT SITE 12 12 BY SIMILARITY. |
| ACT SITE 11 12 BY SIMILARITY. |
| ACT SITE 11 19 BY SIMILARITY. |
| ACT SITE 11 10 BY SIMILARITY. |
| ACT SITE 11 10 BY SIMILARITY. |
| ACT SITE 11 11 BY SIMILARITY. |
| ACT SITE 11 BY SIMILARITY. |
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| ACT SITE 11 BY SIMILARITY. |
| ACT SIMILARITY. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RnaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Papio hamadryas (Hamadryas baboon)
                                                                                                                                       TIŜSUB=Pancreas;
MEDLINE=77065676; PubMed=999896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P00656; 1SRN.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecinae; Papio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primate evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                           Myocastor.
NCBI_TaxID=10157;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A00822; NRCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANGI PAPHA
                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8WN64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 CKDKNTFIYSRPEPVKAIC--KGIIASKNV-LTTFEFYLSDCNATS----RPCKYKLKKS 83
                                                                                                                Flochim. Biophys. Acta 1162:177-186 (1993).

-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and hydrolyzing cellular Endox.

-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
RNASEL OR RNSI.
Myocastor coypus (Coypu) (Nutria).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00092; RNASE Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
MEDLINE=93192291; PubMed=8448182;
Bond M.D., Strydom D.J., Vallee B.L.;
"Characterization and sequencing of rabbit, pig and mouse
angiogenins: discernment of functionally important residues and
                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANGIOGENIN.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06944260BB764938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.4%; Score 113.5; DB 1; 34.2%; Pred. No. 2.5e-05; iive 11; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF00074, rnaseA, 1.
PRINTS, PR00794, RIBONUCLEASE.
ProDom, PD000535, RNaseA, 1.
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MGD; MGI:88022; Ang.
InterPro; IPR001427; RNaseA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC055355; AAH55355.1;
PIR; A35932; A35932.
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promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and manignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                             EMBL; AF441666; AAL61648.1; -.

InterPro; IPR001427; RNaseA.

Pfam; PR00074; rnaseA; 1.

PRINTS; PR000794; RIBOROLIEASE.

ProDom; PD000535; RNASeA; 1.

SMART; SM00092; RNASE Pc; 1.

SMART; SM00092; RNASE Pc; 1.

Hydrolase; Nuclease; Endonuclease; Angiogenesis; Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.

SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                            ANGIOGENIN.
PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.3%; Score 112.5; DB 1; Length 146; ilarity 27.7%; Pred. No. 3.2e-05; Conservative 16; Mismatches 34; Indels 23;
                                                                                 -!- SIMILARITY: Belongs to the pancreatic ribonuclease family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 BY SIMILARITY.
16432 MW; A4C3CED1482370FE CRC64;
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Matches
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Search completed: May 7, 2004, 21:53:04 Job time: 5.30402 secs

6 TFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAIC---KGIIASKNV-LTT 61

| :::[||: 53 TMRRRHLTSP-----

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model OM protein - protein search, 7, 2004, 21:25:55 ; Search time 44.363 Seconds May Run on:

(without alignments)
662.376 Million cell updates/sec

US-09-961-400-11 Title: Perfect score:

1 SDWLJFQKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues Searched:

length: 0 length: 2000000000 DB sed DB sed Maximum I

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq\_29Jan04:\* 1: geneseqp1980s:\* 2: geneseqp1990s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2001s:\* geneseqp2000s:\* geneseqp2002s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

# STIMMARTES

	tion	0 Recombina	'1 Recombina	5 Rana pipi		'9 Rana pipi		9 Recombina	4 Antitumou	α,	D.	5 R. pipien	Ä.	<u>α</u>	ч.	Pro	-	86 Protein d	55 Onconase	13 Antitumou	11 Recombina	33 Rana pipi	22 Frog onco		50 Northern	23 R. pipien
	Description	Aay28870	Aay28871	Aay28865	Aay28867	Aay28879	Aay28866	Aay28869	Aaw06544	Aaw35118	Aaw35134	Aaw35135	Aaw35133	Aaw35129	Aaw35132	Aar12344	Aar47303	Aaw00736	Aaw14065	Aaw06543	Aaw30301	Aaw88233	Aay33322	Aab31666	Abg32650	Aaw35123
SUMMAKIES	ΩI	AAY28870	AAY28871	AAY28865	AAY28867	AAY28879	AAY28866	AAY28869	AAW06544	AAW35118	AAW35134	AAW35135	AAW35133	AAW35129	AAW35132	AAR12344	AAR47303	AAW00736	AAW14065	AAW06543	AAW30301	AAW88233	AAY33322	AAB31666	ABG32650	AAW35123
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de	Query Match I	100.0	100.0	99.3	99.3	99.3	98.8	98.8	96.4	96.2	96.2	96.2	96.2	96.2	96.2	95.5	95.5	95.5	95.5	95.5	95.5	95.5	95.5	95.5	95.5	95.5
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AAW35122 AAW35117 AAW35125 AAW35125	AAW35126 AAW35116 AAW30302	AAY39400 AAW18224 AAW35115	AAW35127 AAW35131 AAB31667	ABG31617 AAW35120 AAW35128	AAW35121 AAW35119 AAW88234 AAY33321
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22 2 2 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	დ	36 37 38	39 40 11	4 4 4 4 2 6 4 2

#### ALIGNMENTS

AAY28870 standard; protein; 104 AA RESULT 1 AAY28870 

AAY28870;

(first entry) 25-JAN-2000 Recombinant RaPLR1 Gln1Ser amino acid sequence.

Recombinant Rana pipiens ribonuclease; RaPLR1 Gln1Ser; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; frog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase; autoimmune disease.

Rana pipiens. Synthetic.

/note= "Wild type Gln replaced with Ser" Location/Qualifiers Misc-difference

07-OCT-1999.

WO9950398-A2

99WO-US006641. 26-MAR-1999; 98US-0079751P 27-MAR-1998; (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Newton DL; Rybak SM,

WPI; 1999-610847/52. N-PSDB; AAZ08128

for e.g. New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.

Claim 34; Page 60; 71pp; English.

The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Gln1Ser. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant Met(-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be tused in-frame with ligand binding moieties to form cytocoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                        1 SDWLTFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                   SDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
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0
                                                                                                                                                Length 104;
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                                                                                                                                                                                                                                                                    SEFYLSDCNVISRPCKYKLKKSINIFCVICENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                          SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENOAPVHFVGVGHC 104
                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RaPLR1 Gln1Ser amino acid sequence.
                                                                                                                                   Score 577; DB 2; Pred. No. 7e-62; O;
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                                                                                                                                                                            .,
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                                                                                                                                                                            Conservative
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                                                                                                                                                           Local Similarity
                                                                                                             Sequence 104 AA;
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                                                                                                                                                                          Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              AAY28871;
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                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rana pipiens liver ribonuclease, RaPLR1; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog; human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant ribonucleases, used for killing target cells, e.g. for ating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                             SDWLTFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                   SDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows t proteins to be fused in-frame with ligand binding moieties to form cytocxic fusion proteins. They can be used for treatment of cancer
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                                                                                                                                             Length 105;
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                                                                                                                                                                                                                                                                                                                SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                    61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                              DB 2;
                                                                                                                                             577; DB 2
No. 7e-62;
                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rana pipiens liver ribonuclease (RaPLR1)
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                                                                                                                                             100.0%; Score 100.0%; Pred.
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                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 104; Conservative
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                                                                        autoimmune diseases
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EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104

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The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Met at position 1. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding motety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadocrophin (hCd) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
0;
                                                                                                                                                                                                                                                                                                                                             Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                61
                                                    2 DWLIFPQKKHITNIRDVDCNNIMSINLFHCKDKNITFIYSRPEFVKAICKGIIASKNVLTIS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                              2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Met not found in wild type RaPLR1"
   Indels
                                                                                                                    62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                               62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
   0;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 34; Page 57; 71pp; English
                                                                                                                                                                                                                  AAY28867 standard; protein; 105
   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0079751P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US006641
                                                                                                                                                                                                                                                                                                                Recombinant Met(-1) RaPLR1
                                                                                                                                                                                                                                                                                  (first entry)
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ08126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9950398-A2
                                                                                                                                                                                                                                                                                 25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                    AAY28867;
      Matches
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                                                                                                                                                                                                                                    LL2 artibody, ligand binding moiety; CD22; cancerous B cell; onconase; Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer; recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                      Rana pipiens ribonuclease Clone Salb; RaPLR1; covalently bound; RNase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Rana_pipiens_Clone_5alb_ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.3%; Score 573; DB 2; Lu
ilarity 100.0%; Pred. No. 2.7e-61;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                         1. .23
/label= Signal_peptide
/note= "Putative"
                                                                                                                                                                                           Rana pipiens Clone 5alb ribonuclease.
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 69; 71pp; English.
                                                                                              Ź
                                                                                              AAY28879 standard; protein; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US006641.
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                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999-610847/52.
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Matches 103; Conserv
                                                                                                                                                                                                                                                                                           autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-610847/
N-PSDB; AAZ08136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1998;
                                                                                                                                                                                                                                                                                                                           Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09950398-A2
                                                                                                                                                           25-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                AAY28879;
                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                               Key
                                                                 RESULT 5
                                                                                  AAY28879
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Match 105; Deal Similarity 100.0%; Pred. No. 2.2e-61; Length 105; Pred. No. 2.2e-61; les 103; Conservative 0; Mismatches 0; Indels

Sequence 105 AA;

diseases

Query Match

Matches

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Sat May

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Recombinant Rana pipiens ribonuclease; RaPLR1 Met23Leu; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Met23Leu. Carboxy terminal end of recombinant RaPLR1 has a covalently bound aligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion preteins. They can be used for treatment of cancer and autoimmune
        61
                                    84
DWLTFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKALCKGIIASKNVLTTS
                    New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 570; DB 2; Length 104;
Pred. No. 4.9e-61;
1; Mismatches 0; Indels
                                                                        EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                 Recombinant RaPLR1 Met23Leu amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                 AAY28866 standard; protein; 104
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                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 34; Page 56; 71pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                     autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                      Key
Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                               Rana pipiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9950398-A2
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                                                                                                                                                                              AAY28866;
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Best Local (
                                                                                                                         RESULT 6
                                                                                                                                         AAY28866
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The present sequence is a recombinant Rana pipiens ribonuclease protein (RaPLR1) with Met at position 1 attached to (His)6 tag and Met241eu. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding molety, which can be a LL2 antibody directed against CD2 on against Kaposi's sarcoma cells. Recombinant ribonucleases can be against Kaposi's sarcoma cells. Recombinant ribonucleases can be presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                           note= "(His)6 histidine tag attached to N-terminal Met"
                                                                                                                                                                                                           Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase; cancerous B cell, Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                     "Met not found in wild type RaPLR1"
        104
                /note= "Wild type Met replaced with Leu"
 62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                                                               Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                 AAY28869 standard; protein; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 59; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US006641.
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                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 105 AA;
                                                                                                                                                                                                                                                                                              Rana pipiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-1999;
                                                                                                                                                       25-JAN-2000
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                                                                                                                           AAY28869;
                           62
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19

DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS

98.8%; Score 570; DB 2; Length 105; llarity 99.0%; Pred. No. 5e-61; Conservative 1; Mismatches 0; Indels

Query Match Best Local Similarity Matches 102; Conserv

0;

Gaps

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19 19

DWLIFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 

Matches 102; Conservative

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Similarity

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AAW35115 to AAW35123 encode recombinant proteins (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablantion by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nonc and also lower
                                                                                                                                                                                                                                                                                                                                                                   Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SDWLTFQXKHLTNTRDVDCNN1MSTNLFHCKDKNTF1YSRPEPVKAICKGIIASKNVLTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 SDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIXSRPEPVKALCKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
             RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.2%; Score 555; DB 2; Length 11.
96.2%; Pred. No. 3.6e-59; Aniematches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCBNQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R. pipiens recombinant RNase rOnc fusion protein 10.
                                                                                                                                                                                                                                                                                  Wlodawer A;
                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Page 63; 90pp; English.
                                                                                                                                                                                                                                                                                  Boque L,
                                                                                                                                                                            97WO-US002588.
                                                                                                                                                                                                              96US-0011800P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW35134 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour cell growth; frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunogenicity in humans
                                 tumour cell growth; frog
                                                                                                                                                                                                                                                                                      Newton DL,
                                                                                                                                                                                                                                                                                                                       WPI; 1997-435168/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT94955
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Synthetic.
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                                                                                                                                                                              19-FEB-1997;
                                                                                                                                                                                                                21-FEB-1996;
                                                                   Rana pipiens
                                                                                                       WO9731116-A2
                                                                                                                                           28-AUG-1997.
                                                                                                                                                                                                                                                                                      Rybak SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW35134;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW1224, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW06543) that have been isolated from Rana pipiens occytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy and surgery in the treatment of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DWLIFQXKHLINIRDVDCNNIMSINLFHCKDXNIFIYSRPEPVKAICKGIIASKNVLITS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
 DWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DWLTFQKKHVTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASRNVLTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 556; DB 2; Length 104;
Pred. No. 2.5e-59;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                          R. pipiens recombinant RNase protein NLSMetSerrOnc.
                                                                                                                                                                                                                                                                          Antitumour protein from Rana pipiens oocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                              Iumour; chemotherapy; radiotherapy; frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein; 112 AA.
                                                                                                                                                                   AAW06544 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 28; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.4%;
97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US008304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                      Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                      WO9639428-A1
                                                                                                                                                                                                                                          22-AUG-1997
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                                         62
                                                                                                                                                                                                       AAW06544;
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Gaps ;

Length 112;

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AAW35133
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                                                                                                                                                                                                                                                                               Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R. pipiens recombinant RNase rOnc fusion protein 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 555; DB 2;
Pred. No. 1e-58;
                                                                                                                                                                       Wlodawer A;
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                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                        English.
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                                                                                                                                                                       Boque L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lower immunogenicity in humans
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                          97WO-US002588,
                                                                      96US-0011800P
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96.2%;
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                                                                                                                                                                  Newton DL,
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                                                                                                                                                                                                              1997-435168/40.
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Les 100; Conser
                                                                                                                                                                                                                                    N-PSDB; AAT94972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 251 AA;
                        19-FEB-1997;
                                                                   21-FEB-1996;
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Synthetic.
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                                                                                                                                                                Rybak SM,
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Matches
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Sequences AAW35125 to AAW35135 represent recombinant fusion proteins (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins ribonucleases have increased cytotoxic activity compared to none also
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                                                   Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                  96.2%; Score 555; DB 2; Length 254; 96.2%; Pred. No. 1e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                           Disclosure; Page 77; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW35133 standard; protein; 355 AA
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                                                                                                                                                                                                                                                                                                                                                lower immunogenicity in humans
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Matches 100; Conservative
WPI; 1997-435168/40.
N-PSDB; AAT94973.
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 254 AA;
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Synthetic.
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ribonucleases have increased cytotoxic activity compared to nonc and also

lower immunogenicity in humans

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novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nonc and also
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          (nonc)
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which are modifications of the RNase Onconase (RTM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 555; DB 2;
Pred. No. 1.6e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wlodawer A;
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                                                                                                                                                                                                                                                                                                                                                                 lower immunogenicity in humans
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96.2%;
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Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 355 AA;
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                     ronc)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells.
                                                                                                                                             252 SDWLTFQKKHITNITRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKOVLTT 311
                                                                                                                  SDWLTFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKALCKGIIASKNVLTT 60
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                                                                                                                                                                                              SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                 R. pipiens recombinant RNase rOnc fusion protein 8.
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Pred. No. 1.6e-58;
2; Mismatches 2;
                                                               Score 555; DB 2;
Pred. No. 1.6e-58;
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                                                                                          2; Mismatches
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                                                                                                                                                                                                                                                                                  AAW35132 standard; protein; 366
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ilarity 96.2%;
Conservative
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                                                                 96.2%;
96.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                               tumour cell growth; frog
                                                                                               Matches 100; Conservative
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ses 100; Conserv
                                                                                Local Similarity
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                                        Sequence 355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rana pipiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9731116-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                  61
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                                                                    Query Match
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Matches
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(ronc) which are modifications of the RNase Onconase (RTM) (fonc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjudates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation fitto a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new

Sequences AAW35125 to AAW35135 represent recombinant fusion proteins

Disclosure; Page 71; 90pp; English

tumour cells.

particularly

WPI; 1997-435168/40.

N-PSDB; AAT94967

Ribonuclease molecules based on native Onconase - used for killing cells,

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The protein is derived from fertilised frogg eggs. It has an iso-electric point of 9.5 - 10.5, a blocked N-terminal gp. and is free of carbohydrates. It is active against certain cancer cells. The combination butene) of the protein and (z-1-p-dimethylaminoethoxyphenyl-1, z-diphenyl-1-separate entities against human pancreatic ASPC-1 adenocarcinoma, and the combination of protein and (10-[3-(4-methyl piperazin-1-yl)-propyl]-2-separate entities against human pancreatic ASPC-1 adenocarcinoma, and the trifluoromethylphenothiazine (Stelazine) is much more reactive than the been shown against human lung A-549 carcinoma. Activity has also been shown against human sub- maxilliary epidermoid carcinoma A-253 HL-60 cells, human colo 320 DM carcinoma IOX melanoma and human lung adumnent colo 320 DM carcinoma LOX melanoma and human lung squamous car- cinoma HT-520 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New protein from fertilised eggs of Rana pipiens - active against cancer cells, esp. in combination with Tamoxifen or Stelazine (trifluoro-perazine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.5%; Score 551; DB 2; Length 104; 96.1%; Pred. No. 9.9e-59; ive 2; Mismatches 2; Indels
                                                            SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                              Protein with activity against cancer cells.
                                                                                                                                                                                                                                                                                        Frog eggs; Tamoxifen; Stelazine; cancer.
                                                                                                                                                                  AAR12344 standard; protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Fig 2; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   89US-00436141.
                                                                                                                                                                                                                                                                                                                                                                                                                                               89US-00436141.
90US-00526314.
                                                                                                                                                                                                                               08-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ardelt WJ, Mikulski SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ALFA-) ALFACELL CORP.
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Best Local Similarity
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18-MAY-1990;
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                                                                                                                                                                                                AAR12344;
                                                            61
                                                                                         323
                                                                                                                                    RESULT 15
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0; Gaps

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62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104 

7, 2004, 21:38:27 Search completed: May Job time : 44.363 secs

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TELEX: NO. 5728805 Applicable INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201-912-0442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
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204.5
203.5
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Sequence 61, Appl
Sequence 49, Appl
Sequence 57, Appl
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Sequence 32, Appl
                                                                    (without alignments)
445.066 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 64,
Sequence 55,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13,
                                                                                                            577
1 SDWLTFQKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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                                                         May 7, 2004, 21:28:45 ; Search time 12.0636 Seconds
                                                                                                                                                                                                                                                                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-467-955-2
US-08-875-811-59
US-08-875-811-65
US-08-875-811-67
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US-09-071-672-11
US-09-071-672-11
US-09-67-748-11
US-09-67-748-11
US-09-67-748-11
US-09-67-748-11
US-09-86-119-11
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US-08-875-811-39
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Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum DB
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; Sequence 2, Application US/08467955
; Patent No. 572806
; GENERAL INFORMATION:
    APPLICANT: Ardelt Ph.D, Mojciech J.
    ATTLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM NUMBER OF SEQUENCES: 2
    CORRESPONDENCE ADDRESS: ADDRESSEE: Mark H. Jay, P.A.
    STREET: P.O. Box E CITY. Short Hills
    CITY: Short Hills
    STATE: New Jersey
COUNTRY: USA
             Sequence
                                                                                                                                                          Sequence
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                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                        Sequence
US-08-626-288-2
US-09-095-429-2
US-08-875-811-24
US-08-875-811-24
US-09-394-268-2
US-09-394-268-2
US-09-387-811-20
US-08-875-811-20
US-08-875-811-20
US-08-875-811-22
US-08-875-811-22
US-09-875-811-22
US-09-86-119-3
US-09-986-119-3
US-09-986-119-3
US-09-986-118-3
US-09-986-118-4
US-09-223-118-4
US-09-223-118-4
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APPLICATION NUMBER: US 07/178,118

FILING DATE: 06-APE-1988

FRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141

FILING DATE: 13-NOV-1989

FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332

RIUNG APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970

FILING DATE: 01-REB-1992

RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970

FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAMME: JAY, MARK H.

REGISTATION NUMBER: 27507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07078-0383
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/467,955
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                                    1 SDWLTFOKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
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                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rybar, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Liluis
APPLICANT: Middawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.2%; Score 555; DB 3; Length 251; 96.2%; Pred. No. 1.2e-59; live 2; Mismatches 2; Indels
                                                                                                                                                         SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 112
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DARN:
APPLICATION NUMBER: US/08/875,811
FILING DARE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-196
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REGISTRATION NUMBER: 41,739
REGISTRATION NUMBER: 41,739
REGISTRATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                      ; Sequence 59, Application US/08875811; Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 96.2
Matches 100; Conservative
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LENGTH: 251 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Embarcad
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                    US-08-875-811-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-875-811-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-08-875-811-61
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                                                                                                                                                                                                                                                                                 2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                       2 DWLTFQKKHVINIRDVDCNNIMSTNLFHCKDKNYFFIYSRPEPVKAICKGIIASKNVLTTS
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                                                                                                                                                                                                  Score 556; DB 1; Length 104;
Pred. No. 2.8e-60;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.2%; Score 555; DB 3; Length 112; 96.2%; Pred. No. 4.1e-60; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                     62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                  EFYLSDCNVISRPCKYKLKKSTNKFCVICENQAPVHFVGVGRC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INTENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STRAET: California COUNTRY: USA LIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk COMPUTER: IBM PC compatible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PULDADALICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY: ABENT: 11-FEB-1996
ATTORNEY: SUSAN K.
NAME: Faris, Susan K.
NAME: Faris, Susan K.
FRGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
                                                                                            OMGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Occyte
US-08-467-955-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 01.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           Query Match
Best Local Similarity 97.1%;
Matches 100; Conservative
                                    ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 amino acids
protein
N
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Best Local Similarity 96.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-32
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MOLECULE TYPE:
HYPOTHETICAL:
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Gaps

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19-FEB-1998
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ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 355 amino acids
amino acid
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                California
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                                       USA
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Matches 100;
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                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 49, Application US/08875811
; Sequence No. 6045793
; Patent No. 6045793
; Patent No. 6045793
; APPLICANT: Ryback, Susanna M.
APPLICANT: Newton, Diame L.
APPLICANT: Modawer, Alexander
TILLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                  APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Browe, Lluis
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: TEM PC compatible
CORPETATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTONEY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA
Sequence 61, Application US/08875811 Patent No. 6045793
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 96.2
Matches 100; Conservative
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                                Patent No. 6045793
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-875-811-49
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CONFITE 1911-1934

CONFITE STATE 1911-1934

WEDITHER TENDEN FOR 1911-1934

WEDITHER THE FLORY disk, 1911-1934

WEDITHER THE FLORY disk, 1915-1959

CONFIDENT APPLICATION DATA 155

CONFIDENT OF 1911-1959

APPLICATION NUMBER: US 60'011,800

FILING DATE: 19-FEB-1998

APPLICATION NUMBER: US 60'011,800

FILING DATE: 19-FEB-1999

APPLICATION NUMBER: US 60'011,800

FILING DATE: STATE 19-FEB-1999

APPLICATION NUMBER: US 60'01,800

APPLICATION NUMBER: MATERIAL NUMBER: US 60'01,800

APPLICATION NUMBER: US 60'01,800

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252 SDWLIFEQKKHITUTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLFT 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.2%; Score 555; DB 3; Length 35 96.2%; Pred. No. 1.8e-59; 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQADVHFVGVGSC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Lluis
APPLICANT: Modawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein

1 COCATION: 1..355

OTHER INFORMATION: /note= "E6FB (Met-(-1)) Serronc"

US-08-975-811-64
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTOREY/AGENT INFORMATION:
AND THE TRANTAL THEORY OF THE TRANTALION:
AND THE TRANTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLI STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-08-875-811-55
; Sequence 55, Application US/08875811
; Patent No. 6045793
                                                                            TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                (415) 576-0200
                                                                                                                                                                             355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.2*
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 576-020
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
: USA
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TOPOLOGY: linear
                                                                                                                                                                                                         TYPE: amino STRANDEDNESS:
                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CA
                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH:
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Pred. No. 1.8e-59;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 SEFYLSDCNVISRPCKYKLKKSTNKFCVICENQAPVHFVGVGSC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Lluis
APPLICANT: Widdawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CLASSIFICATION: 435
PRIOR APPLICATION DATA.
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
RAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
FEFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LEWGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                           015280-244100US
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STATE: Galifornia
CONTRY: USA
ZIP: 9411-3834
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 64, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
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REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.2%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / MOLECULE TYPE: protein US-08-875-811-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Gaps

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2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
96.1%; Pred. No. 1.1e-59;
iive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 104 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal
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                     99; Conservative
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Best Local Similarity
Matches 99; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
Best Local Similarity
Matches 99; Conserv
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FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                         US-07-921-619-1
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                                                                                                                                                  1 SDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn.
STATE: New York
                                                                                                         .
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                                                              96.2%; Score 555; DB 3; Length 366; 96.2%; Pred. No. 1.9e-59; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                       323 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/921,180
APPLICATION NUMBER: US 07/921,180
FILING DATE: 06-APR-1988
FILOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/283,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5006 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELERA: 718-625-0399
TELER: No. 5529775 Applicable INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08283971
Patent No. 5529775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 104 amino acids
amino acid
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DEVELOPMENTAL STAGE: E
                                                                                 Best_Local Similarity 96.2
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: N
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    MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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            ; MOLECOLE ;
US-08-875-811-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-283-971-1
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                                                                Query Match
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DB 1; Length 104;

Score 551;

95.5%;

Query Match

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2 DWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
                                                                                                                                                                                                                                                                                 APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Ardelt Ph.D, Stanislaw M.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 104;
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96.1%; Pred. No. 1.1e-59;
iive 2; Mismatches 2; Indels
                                                                    62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                  62 EFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/921,619
FILING DATE: 19920728
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jay, Mark H.
REGISTRATION WUMBER: 27507
REFERENCE DOCKET NUMBER: 5005 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 718-625-0399
TELEX: No. 5595734 Applicable INFORMATION FOR SEQ ID No: 1: SEQUENCE CHARACTER:
                                                                                                                                                                                                                                Sequence 1, Application US/07921619
Patent No. 5595734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OKGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Embryo
US-07-921-619-1
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2 DWLTFQKKHITNTRDVDCDNIMSTNLFFCKDKNTFIYSRPEPVKAICKGIIASKQVVLTTS
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                                                                                                                                                                                                            Sequence 13, Application US/08891848
Fatent No. 5955073
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Rolle, Richard J.
APPLICANT: Nowton, Diame L.
APPLICANT: Newton, Diame L.
APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 104;
                                        EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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/note= "Onconase from Rana pipiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OMPUTER: IBM PC Compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,848
FILING DATE: No. 5955073 yet assigned
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/125,462
FILING DATE: 22-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/014,082
FILING DATE: 22-SEP-1993
PRIOR APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-CT-1991
PRIOR APPLICATION NUMBER: US 07/779,195
FILING DATE: 20-APR-1990
PRIOR APPLICATION NUMBER: US 07/779,195
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INPORMATION:
NAME: WEBEY, BILLEN LAUVER
NAME: WEBEY, BILLEN LAUVER
REGISTRATION NUMBER: 32,762,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: Townsend and Townsend and Crew LLP
F: Two Embarcadero Center, Eighth Floor
San Erancisco
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.5%; Score 551; DB 2; I
llarity 96.1%; Pred. No. 1.1e-59;
Conservative 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   015280-110310US
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TELEFAX: (415) 576-0200
: INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amiliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111-3834
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                           US-08-891-848-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-891-848-13
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62
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Best Local S
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                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.A.
STREET: P.O. Box E
CITY: Short Hills
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 104;
                                                         EFYLSDCHVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                 EFYLSDCNVISRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
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96.1%; Pred. No. 1.1e-59;
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION ADM:
APPLICATION NUMBER: US 07/178,118

FILING DATE: 06-APR-1988

FILING DATE: 06-APR-1988

FILING DATE: 13-NOV-1989

FILING DATE: 13-NOV-1989

FILING DATE: 13-NOV-1989

FILING DATE: 03-FBE-1922

FILING DATE: 03-FBE-1922

FILING DATE: 03-FBE-1932

FILING DATE: 01-RES-1934

ATOMNEY APPLICATION NUMBER: US 08/283,970

FILING DATE: 01-AUG-1994

ATOMNEY APPLICATION NUMBER: 27507

RESERENCE/DOCKET NUMBER: 27507

RESERENCE/DOCKET NUMBER: 27507

RESERENCE/DOCKET NUMBER: 27507

RESERENCE/DOCKET NUMBER: 27507

TELECOMMUNICATION NUMBER: 27507

TELEFAK: 201-912-9066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              Sequence 1, Application US/08467955
Patent No. 5728805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: No. 5728805 Applicable INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Rana pipiens
) DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New Jersey
COUNTRY: USA
ZIP: 07078-0383
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 96.1'
Matches 99; Conservative
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FRAGMENT TYPE: 1
ORIGINAL SOURCE:
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SEQ ID NO 1
LENGTH: 104
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                                                                                                                                                                                                                                                       Sequence 1, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
APPLICANT: Wodawer, Alexander
APPLICANT: Boque, Lluis
APPLICANT: Wodawer, Alexander
APPLICANT: Wodawer, Alexander
APPLICANT: Wodawer, Alexander
APPLICANT: Requested and Crew LLP
CORRESPONDENCE ADDRESS:
CORRESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "native ONCONASE (Registered
62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                 62 EFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
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US-08-875-811-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trademark) from Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FFB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRICE APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRICE APPLICATION NUMBER: WS 60/011,800
FILING DATE: 21-FEB-1996
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
APPLICATION NUMBER: 41,739
REGISTATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 012280-244100US
TELEPHONE: (415) 576-0300
TELEPAX: (415) 576-0300
INFORMATION FOR SEC 1D NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.5%; Score 551; DB ilarity 96.1%; Pred. No. 1.1e Conservative 2; Mismatches
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OTHER INFORMATION: /label= nonc
OTHER INFORMATION: /note= "natis
OTHER INFORMATION: Trademark) fi
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TYPE: amino acid
STRANDEDNESS:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
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Best Local Similarity
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                                                                                                                                                                                                     RESULT 13
US-08-875-811-1
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62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104

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2 DWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
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                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
APPLICATION: WUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
TITLE OF INVENTION: MAKING THEM
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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| Sequence 1, Application US/09071672
| Patent No. 6395276
| GENERAL INFORMATION:
| APPLICANT: Ryback, Susanna M. APPLICANT: Nowton, Dianne L. APPLICANT: Goldenberg, David M. TITLE OF INVENTION: Immunotoxins Directed Against Malignant TITLE OF INVENTION: Cells
| NUMBER OF SEQUENCES: | CORRESPONDENCE ADDRESSE: | CORRESPONDENCE ADDRESSE: | CORRESPONDENCE MADDRESSE: | CORRESPONDENCE MAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.5%; Score 551; DB 3; Length 104; 96.1%; Pred. No. 1.1e-59; ive 2; Mismatches 2; Indels
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62 BFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
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SOUTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,672
FILING DATE: 01-MAY-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,895
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Bllen Lauver
REGISTRATION NUMBER: 32,762
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TELEPAX: (415) 576-0300
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MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/09394268
; Patent No. 6175003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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ZIP: 94111-3834
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| SEQUENCE HEARCTERISTICS:
| SENGETH: 104 amino acids | TYPE: amino acid | TYPE: protein | TOGATION: 1 | TOGATION: | TO
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Search completed: May 7, 2004, 21:40:44 Job time : 12.0636 secs

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May 7, 2004, 21:29:40; Search time 33.3695 Seconds (without alignments) 865.070 Million cell updates/sec
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1 SDWLIFQKKHLINTRDVDCN.....TFCVICENQAPVHFVGVGHC 104
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| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_pep:*
3: cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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7: cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_pep:*
11: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1140673 seqs, 277566755 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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                                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 11, Appl	Sequence 11, Appl	Sequence 13, Appl	Sequence 13, Appl		Sequence 6, Appli	~	Sequence 28, Appl		Sequence 9, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 8, Appli	Sequence 8, Appli
SUMMARIES	ΩΙ	US-09-948-391A-11	US-09-961-400-11	US-09-948-391A-13	US-09-961-400-13	US-09-961-400-2	US-09-948-391A-6	US-09-961-400-6	US-09-948-391A-28	US-09-961-400-28	US-09-961-400-9	US-09-948-391A-2	US-09-948-391A-4	US-09-961-400-4	US-09-961-400-8	US-09-948-391A-8
		10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
	% Query Match Length DB	104	104	105	105	104	105	105	127	127	111	104	104	104	105	105
	* Query Match	100.0	100.0	100.0	100.0	99.3	99.3	99.3	99.3	99.3	98.8	7.76	97.7	7.76	97.1	96.2
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Sequence 9, Appli Sequence 1, Appli	(n)	٠,		Sequence 3, Appli		•••	equence ;	•	•		Sequence 15, Appl		19,	N	21,	22	Sequence 22, Appl	Н	19	7	8	Sequence 139, App	Sequence 5, Appli	0	Sequence 6, Appli	Α,	254	Sequence 254, App
10 US-09-948-391A-9 9 HS-09-986-119-1	10 US-09-918-887-1		12 US-10-461-713-53	9 US-09-986-119-3	10 US-09-918-887-3	10 US-09-948-391A-24	US-09-961-4	-60-SD	-60-SN	10 US-09-948-391A-15		US-09-961	10 US-09-961-400-19	10 US-09-948-391A-21	10 US-09-961-400-21	10 US-09-948-391A-22	10 US-09-961-400-22		10 US-09-948-391A-19		12 US-10-016-248-89		13 US-10-016-447-5	US-1	9 US-09-286-240-6	9 US-09-863-777-2	09-731-872-2	10 US-09-876-997-254
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16	- 88 - 17	19	20	21	22		24 2	25 2	26 2					31 2				35 2			38	39		41	42	43	44	45

#### ALIGNMENTS

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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
OTHER INFORMATION: ribonuclease with Gln1Ser substitution
OTHER INFORMATION: (recombinant RaPLR1 Q1S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 577; DB 10; Length 104; 100.0%; Pred. No. 1.3e-58; tive 0; Mismatches 0; Indels 0;
     Sequence 11, Application US/09948391A

Sequence 11, Application US/09948391A

Publication No. US20030027311A1

GENERAL INFORMATION:

APPLICANT: Wewton, Dianne L.

APPLICANT: The United States of America

APPLICANT: The United States of America

APPLICANT: The Pepartment of Health and Human Services

TITLE OF INVENTION: Recombinant Anti-Tumor RNase

FILE REPERENCE: 015280-343110US

CURRENT FILING DATE: 2002-05-10

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 2000-08-17

WUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

FEMALE APPLICATION VOWER: US 09/622,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 104; Conservative
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US-09-948-391A-11
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1 SDWLTFQXKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKALCKGIIASKNVLTT 60

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ORGANISM: Rana pipiens
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US-09-961-400-13
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Best Local 2
                   FEATURE:
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APPLICANT: RYBAK, SUSANNA M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

TITLE OF INVENTION: INMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT TITLE OF INVENTION: CELLS.

FILE REFERENCE: 018733/1059

CURRENT APPLICATION NUMBER: 09/622,613

FRIOR APPLICATION NUMBER: 09/622,613

FRIOR APPLICATION NUMBER: PCT/US99/06641

FRIOR APPLICATION NUMBER: ECT/US99/06641

FRIOR APPLICATION NUMBER: 66/079,751

FRIOR PILING DATE: 1999-03-26

FRIOR PILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.1

**SEQ ID NO 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
1 SDWLIFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
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                                                   SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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APPLICANT: Newton, Dianne i.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: Bepartment of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-34310US
CURRENT APPLICATION WUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTING UNIVER: US
SOFTWARE: PATENTING UNIVER: US
LENGTH: 105
THENCH APPLICATION NUMBER: US
SOFTWARE: PATENTING UNIVER: US
SOFTWARE: PATENTING UNIVER: US
SOFTWARE: PATENTING UNIVER: US
SOFTWARE: PATENTING UNIVER: US
SEQ ID NO 13
THENCH: 105
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Publication No. US20030027311A1
                                                                                                                                                                                                               Sequence 11, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
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US-09-948-391A-13
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Sequence 13, Application US/09961400
| Publication No. US20030124131A1
| GENERAL INFORMATION:
| APPLICANT: STBAK, SUSANNA M.
| APPLICANT: GOLDENBERG, DAVID M.
| APPLICANT: MEWION, DIANNE L.
| TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT: TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT: TITLE OF INVENTION: UNBER: US/09/961,400
| FILE REFERENCE: 018733/1059
| CURRENT FILING DATE: 2001-09-25
| PRIOR APPLICATION NUMBER: 09/622,613
| PRIOR APPLICATION NUMBER: 09/622,613
| PRIOR PILING DATE: 1999-03-26
| PRIOR FILING DATE: 1999-03-26
| PRIOR FILING DATE: 1999-03-26
| PRIOR FILING DATE: 1999-03-26
| WINNERD OF SED IN NUMBER: 60/079,751
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Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: CELLS
FILLE REFERENCE: 019733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
                                                                                                                                                                                                                                                      1 SDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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CTHER INFORMATION: Description of Artificial Sequence: Rana pipiens OTHER INFORMATION: ribonuclease with Met at position 1 and Gln2Ser CTHER INFORMATION: substitution (recombinant Met(-1) RapERI QLS) US-09-948-391A-13
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                                                                                                                                                 Length 105;
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                                                                                                                                                                                                                                                                                                                                                                       61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                           100.0%; Score 577; DB 10; 100.0%; Pred. No. 1.3e-58;
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                                                                                                                                                                                                       0; Mismatches
                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 104; Conservative
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SEQ ID NO 13
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Query Match 99.3%; Score 573; DB Best Local Similarity 100.0%; Pred. No. 3.8 Matches 103; Conservative 0; Mismatches
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Sequence 6, Application US/09961400 Publication No. US20030124131A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 127
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; ORGANISM: Rana pipiens
US-09-961-400-6
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99.3%; Score 573; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 3.8e-58;
Matches 103; Conservative 0; Mismatches 0; Indels
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APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Serpresented by The Secretary of the
APPLICANT: Serpresented by The Secretary of the
APPLICANT: Serpresented by The Secretary of the
APPLICANT: Obsartment of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE OF INVENTION: Recombinant Anti-Tumor RNase
CURRENT APPLICATION NUMBER: US 00/079,751
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR PLING DATE: 1999-03-27
PRIOR PLING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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Best Local Similarity 100.0%; Pred. No. 3.8e-58;
Matches 103; Conservative 0; Mismatches 0;
     PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1939-03-26
PRIOR FILING DATE: 1939-03-26
PRIOR FILING DATE: 1938-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.1
SSQ ID NO 2
LENGTH: 104
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                      ; ORGANISM: Rana pipiens
US-09-961-400-2
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RESULT 7 US-09-961-400-6

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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, BUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: LAGORICAN CONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: LOSINGS: 01873/1059
CURRENT APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: POT/US99/06641
PRIOR APPLICATION NUMBER: POT/US99/06641
PRIOR APPLICATION NUMBER: POT/US99/06641
PRIOR PILING DATE: 1999-03-26
PRIOR PILING DATE: 1999-03-26
PRIOR PILING DATE: 1998-03-26
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PRIOR PILING DATE: 1098-03-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.3%; Score 573; DB 10; Length 105; 100.0%; Pred. No. 3.8e-58;
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APPLICANT: The United States of America
TITLE APPLICANT: Separate of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR PRILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
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Best Local Similarity 99.0
Matches 102; Conservative
                ORGANISM: Rana pipiens
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Best Local Similarity
Matches 102; Conserv
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                ; UKGRALL.
US-09-961-400-9
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US-09-948-391A-4
                                                                        Query Match
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                                                                                                                                                                                                        Sequence 28, Application US/09961400

Publication No. US20030124131A1

GENERAL INFORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: HENTON, DIANNE L.

ITILE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT APPLICATION NUMBER: US/09/25,613

FRIOR APPLICATION NUMBER: O9/622,613

PRIOR FILING DATE: 2000-09-12

FRIOR APPLICATION NUMBER: 60/7/US99/06641

FRIOR APPLICATION NUMBER: 60/079,751

FRIOR APPLICATION NUMBER: 60/079,751

FRIOR APPLICATION NUMBER: 60/079,751

FRIOR APPLICATION NUMBER: 60/079,751

FRIOR PELING DATE: 1998-03-26

SOFTWARE: PARENT IN VET: 2.1

SEQ ID NOS: 43

LENGTH: 127
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Publication No US20030124131A1

GENERAL INPORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: GULDENBERG, DAVID M.

APPLICANT: GULDENBERG, DAVID M.

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

FILE REFERENCE: 018733/1059

CURRENT APPLICATION NUMBER: 09/62,613

FRICE REPLICATION NUMBER: 09/622,613

PRIOR FILING DATE: 1099-03-26

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN UNER: 07.05.25

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 9

TYPE: PRICE
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                                2 DWLTFQKKGHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
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DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKALCKGIIASKNVLTTS
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                                                                              EFYLSDCNVTSRPCKYKLKKSTNTFCVTCBNQAPVHFVGVGHC 104
                                                                                                       Indels
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99.3%; Score 573; DB 10;
Best Local Similarity 100.0%; Pred. No. 4.8e-58;
Matches 103; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT

ORGANISM: Rana pipiens
US-09-961-400-28
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US-09-961-400-9
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                                                                                                           2 DWLTFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
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           Length 111;
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                                                          0; Indels
                                                                                                                                                                                                                  62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERRNCE: 015280-343110US
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR PILING DATE: 1999-03-26
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 43
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Publication No. US20030027311A1

GENERAL INFORMATION:
APPLICANT: Wybak, Susama M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Department of Health and Human Services
TITLE REFERENCE: 01520-343110US

FILE REFERENCE: 01520-343110US

CURRENT APPLICATION NUMBER: US/09/948,391A
     DB 10;
  Score 570; DB 10
Pred. No. 9e-58;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: ribonuclease (RaPLR1) US-09-948-391A-2
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09948391A; Publication No. US20030027311A1; GENERAL INFORMATION:
98.8%;
99.0%;
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Sequence 4, Application US/09961400

Publication No. US20030124131A1

GENERAL INFORMATION:
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: LELIS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/VS99/06641
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER: OF SEQ ID NOS: 43
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 DWLIFQKKHLINIRDVDCNNILSTNLFHCKDKNFFIYSRPEPVKAICKGIIASKNVLITF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DWLTFQKKHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens OTHER INFORMATION: ribonuclease with Met23Leu substitution OTHER INFORMATION: (recombinant RaPLR1 Met23Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 564; DB 10; Length 104;
Pred. No. 4.1e-57;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
97.7%; Score 564; DB 10; Length 104;
Best Local Similarity 98.1%; Pred. No. 4.1e-57;
Matches 101; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR PRILOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
; LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.1%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Rana pipiens
US-09-961-400-4
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-948-391A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 104
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US-09-961-400-4
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RESULT 14 US-09-961-400-8

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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT APPLICATION NUMBER: US/09/622,613
PRIOR APPLICATION NUMBER: CT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1996-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 1.2e-56;
1; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 96.2%; Score 555; DB 10; Length 105; Best Local Similarity 97.1%; Pred. No. 4.5e-56; Matches 100; Conservative 1; Mismatches 2; Indels Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-3431100S
CURRENT FILING DATE: 1908-03-27
CURRENT FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08948391A; Publication No. US20030027311A1; GENERAL INFORMATION:
Sequence 8, Application US/09961400 Publication No. US20030124131A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.1%;
Best Local Similarity 97.1%;
Matches 100; Conservative
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US-09-948-391A-8
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95 Pp 95

62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104

λ α

Search completed: May 7, 2004, 21:51:57 Job time: 34.3695 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein

May Run on:

7, 2004, 21:38:36 ; Search time 9.43686 Seconds (without alignments) 1060.090 Million cell updates/sec

1 SDWLTFQKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104 score: Sequence: Perfect

US-09-961-400-11

Title:

283366 segs, 96191526 residues Gapop 10.0 , Gapext 0.5 Searched:

BLOSUM62

Scoring table:

283366 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB & Maximum DB &

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

precurs ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc angiogenin precurs ribonuclease 4 (EC pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc angiogenin - rabbi pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc ribonuclease-relat ribonuclease-relat pancreatic ribonuc angiogenin [valida pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic-type ri eosinophil-associa pancreatic ribonuc angiogenin - pig ribonuclease Description angiogenin pancreatic SUMMARIES A39035 A27121 JX0120 JX0085 S41111 NRUI A32474 NRCU NRCU NRWKK NRGPB A35932 NRCB NRYY B43825 NRHP \$20066 A43825 JC6159 NRGPA JC6160 I52489 S08549 NRBOB NRPG NRPQ NRBO NRHO Query Match Length DB 124 124 128 150 147 124 19.8 19.6 19.4 287 280.5 264.5 144 132 128 128 126 120 120 119.5 Score Result No.

	pancreatic ribonuc		pancreatic ribonuc												
NRSH	NRPRH	S07141	NRWB	NRGN	NRGF	NRDEO	NRCM	NRCMM	NRCMB	NROW2	NRHY	NRDER	NRDEN	NREKN	NRDEF
н.	Н	N	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	н
124	124	124	124	124	124	124	124	124	124	128	124	124	124	124	124
18.9	18.9	18.9	18.7	18.7	18.5	18.2	18.2	18.2	18.2	18.2	18.0	17.9	17.9	17.9	17.7
109	109	109	108	108	107	105	105	105	105	105	104	103	103	103	102
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C.Species: Rana pipiens (northern leopard frog (Iragment)
C.Species: Rana pipiens (northern leopard frog)
C.Species: Rana pipiens (northern leopard frog)
C.Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C.Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C.Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
R.Ardelt, W. J. Mikulski, S. M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A.Fitle: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl A; Reference number: A39035, MUID:91093131; PMID:1985896
A; Reference number: A39035
A; Ascarus: preliminary
A; Molecule type: protein
A; Residues: 1-104 cARD>
C; Superfamily: pancreatic ribonuclease
                                                    ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
A39035
```

Gaps 0 Length 104; 95.5%; Score 551; DB 2; Length 10 96.1%; Pred. No. 2.1e-48; ive 2; Mismatches 2; Indels 99; Conservative Query Match Best Local Similarity Matches 99; Conserv

. 0

61 61 2 DWLTFQKKHIINTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKRVVLTTS 2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS ð

62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104 Dp à

RESULT 2

ribonuclease-related sialic acid-binding lectin - bullfrog C;Species: Rana catesbeiana (bullfrog) C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993 C;Accession: A27121 R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanagi Biochemistry 26, 2189-2194, 1987 A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana) A;Reference number: A27121; MUID:87299649; PMID:3304421

A; Molecule type: protein A; Residues: 1-111 < TIT> C: Superfamily: pancreatic ribonuclease C; Keywords: lectin

8; Gaps Query Match 49.7%; Score 287; DB 2; Length 111; Best Local Similarity 49.1%; Pred. No. 7.4e-22; Matches 54; Conservative 16; Mismatches 32; Indels

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57 2 NWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 60 2 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV g ð

eosinophil-associa

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guinea-pig: comparison of the
                                                                                                                                                                                  pancreatic ribonuclease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SDWLTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPBPVKAICKG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pancreatic ribonuclease (EC 3.1.27.5) - cuis
NyAlternate names: RNase 1; RNase A
C;Species: Galea musteloides (cuis)
C;Species: G3-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 04-Oct-1996
C;Accession: A00827
R;Beintema, J.J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1983
A;Title: Origin of the duplicated ribonuclease gene in guinea-pig: compariso A;Reference number: A92957; MUID:87036770; PMID:6571219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenin [validated] - bovine
N;Alternate names: angiogenesis factor
N;Contains: ribonuclease (EC 3.1.27.-)
C;Species: Bos primigenius taurus (cattle)
C;Date: 25-Sep-1989 #sequence revision 25-Sep-1989 #text_change 15-Sep-2000
C;Accession: A32474; S02001; A30044; S48212
                                      C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DWSSFQNKHIDYPETSASNPNAYCDLMMQRRNLNPTKCKTRNTFVHASPSEIQQVCGSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 DWLTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAIC--KG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;94/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Indels
                                                                                                                                                                                      (Iguana iguana)
PMID:8307028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-124 <BEI>
A;Note: about one-third of the molecules lacked Ala-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 144; DB 2;
Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.0%; Scor. 30.1%; Pred. No. 1...
                                                                 C; Accession: S41111
R; Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Bur. J. Biochem. 219, 641-646, 1994
A; Title: The amino acid sequence of iguana
A; Reference number: S41111; MUID:94139745; ]
A; Accession: S41111
C; Species: Iguana iguana (common iguana)
                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Moleoule type: profesin
Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Conservative
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Best Local Similarity
Matches 34; Conserv
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PVHF 120
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C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Datession: JX0085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Obg
J. Biochem. 106, 729-735, 1989
A;Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A;Reference number: JX0085, MUID:90130374; PMID:2613682
A;Ancession: JX0085
A;Molecule type: protein
A;Residues: 1-111 ANT:
C;Superfamily: pancreatic ribonuclease
C;Keywords: hydrolase; pyroglutamic acid
C;Keywords: hydrolase; pyroglutamic acid
C;Keywords: hydrolase; pyroglutamic acid
C;Keywords: hydrolase; pyroglutamic acid
C;Mohadiida site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10,35,104/Active site: His, Lys, His #status predicted
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                   C. Date: Lucue, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
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                                                                                                                                                                                                                                                                                                                                 C;Species: Rana japonica (Japanese frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DWLTFQKKHLINTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV
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NWAKFKEKHIRSTSSIDCNTIMDKAIYIGGKCKERNTFIISSEDNVKAICSGVSPDRKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LITSEFYLSDC---NVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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                                                                         LTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
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1 Similarity 42.7%; Pred. No. 1.3e-19;
47; Conservative 19; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Mismatches
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Best Local Similarity
Matches 49; Conserv
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Matches 47; Conserv
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National control of the amin parceatic ribonuclease (EC 3.1.27.5) - capybara
NyAlternate names: RNase 1; RNase A
Cybacies: Hydrochaeris hydrochaeris (capybara, carpincho)
Cybacies: Hydrochaeris hydrochaeris (capybara, carpincho)
Cybacession: Au091984 #sequence_revision 03-Au9-1984 #text_change 29-Oct-1999
Cybacession: Au0824
RyBeintema, J.J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1983
A.Accession: A0191 of the duplicated ribonuclease gene in guinea-pig: comparison of the amin A;Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amin A;Reference number: A92957; MUID:87036770; PMID:6571219
A.Accession: A00824
A.Molecule type: protein
A.Residues: 1-128 ekEI:
C,Superfamily: pancreatic ribonuclease
                                                                                                                                 mature form) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coypu and chinchilla pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           panoreatic ribonuclease (EC 3.1.27.5) - Chinchilla brevicaudata (tentative sequence) N;Alternate names: RNase 1; RNase A C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata (C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000 C;Accession: A00820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 FQKNVPCKNGQSNCYQSNSNAMHITDCRLTSNSKYPNCSYRTSRENKGIIVACEGNPYVPV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDWLTFQKKHL----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKALCKGII 52
C;Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic F;1-24/Domain: signal sequence #status predicted <SIG> F;25-145/Product: angiogenin #status predicted <MAT> F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #statu F;37,64,137/Active site: His, Lys, His #status predicted F;50-104,63-115,81-130/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 KHLINTRDVD------KGIIASKNIF--HCKDKNTFIYSRPEPVKAIC--KGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 KFLTOHHDAKPKGRDDRYCERMMKRRSLTSPCKDVNTFIHGNKSNIKAICGANGSPYREN
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                                                                                                                                                                                                                                                                                                                                                                                       17;
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                                                                                                                                                                                                                                                                                                     Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 LRMSKSPFQVTTCKHTGGSPRPPCQYRASAGFRHVVIACENGLPVHF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.5%; Score 118; DB 1; Length 124; 27.0%; Pred. No. 7.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
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                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 V-LITSEFYLSDCNVTS----RPCKYKLKKSINTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rivan den Berg, A.; van den Hende-Timmer, L.; Beintema, Blochim. Blochys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of A;Reference number: 490612; MUID:77065676; PMID:999896
                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                                                     Score 119.5; DB Pred, No. 6.5e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       12; Mismatches
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30.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                33; Conservative
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A, Molecule type: protein
A, Residues: 1-124 < VAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 HF 120
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R, van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
Ryvan den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
But. J. Blochem. 75, 91-100, 197
A; Pitle: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A; Reference number: A91247; MUD: 77185023; PMID: 862624
A; Accession: A00826
A; Accession: A00826
A; Accession: A00826
A; Note: G-Pro was also found
C; Superfamily: pancreatic ribonuclease
C; Reywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
C; Reywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F; 12, 41, 119/Active site: His, Lys, His #status predicted
F; 24, 41, 418/Active site: Also, Lys, His #status predicted
F; 26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues;Superfamily: pancreatic ribonuclease
                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
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                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                             6 FQKKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nighternate rames: angiogenesis factor
NyContains: ribonuclease (EC 3.1.27.-)
Cypecies: Mus musculus (house mouse)
Cypecies: Mus musculus (house mouse)
Cypecies: Mus musculus (house mouse)
CyAccession: A35932
RyBond, M.D.; Vallee, B.L.
Biochem: Biophys. Res. Commun. 171, 988-995, 1990
A;Reference number: A35932; MUD:91025023; PMID:2222458
A;Accession: A35932
A;Status: not compared with conceptual translation
A;Residues: 1-145 < BON>
A;Residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.Alternate names: RNase IB
C.Species: Cavia porcellus (guinea pig)
C.Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                  64 PCKNGQSNCYESTSNMHITDCRLTSNSKFPDCLYRTSQEEKSIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDWLTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAICKGI
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                                                                                                                                                                                                                                                          A;Cross-references: GB:U22516; NID:9726325; PIDN:AAA91366.1; PID:9726326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     guinea pig (tentative sequence)
                                                                                                                                                                                                                                                                                                                                                             -LITSEFYLSDCNVTSR----PCKYKLKKSTNTFCVTCENQ--APVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.8%; Score 120; DB 1; Length 128; 28.5%; Pred. No. 5.1e-05;
                                      Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                  20.8%; Score 120; DB 1; 29.9%; Pred. No. 5.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Mismatches
                                                                                                                    18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pancreatic ribonuclease (EC 3.1.27.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                    35; Conservative
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Best Local Similarity
Matches 35; Conserv
                              Query Match
Best Local Similarity
Matches 35; Conserv
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9

28 96

> C, Genetics: C; Function:

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A,Molecule type: protein
A,Residues: 1-124 < EMM>
C,Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                        Local Similarity 29.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
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Matches
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NRKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Appertmental source: milk Riocdan, J.F.; Vallee, B.L. submitted to the Brookhaven Protein Data Bank, January 1995
A; Reference number: A65065; PDB:1AGI
A; Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125
B; Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
B; Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
B; A; Title: Crystal structure of bovine angiogenin at 1.5 Angstroms resolution.
A; Reference number: A58315; MUID:95224057; PMID:7708782
A; Contents: annotation; X-ray crystallography, 1.5 angstroms
A; Contents: annotation; C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
B; Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
B; Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
B; Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
B; Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
B; Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
B; Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
B; Contents: annotation; conformation by (1)H-NMR.
B; Reference number: A5881; MUID:9628645; PMID:9688423
A; Contents: annotation; conformation by (1)H-NMR.
B; Rejsdorf, C.; Abergel, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G.
B; R; Rejsdorf, C.; Abergel, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G.; A; Reference number: S48212; MUID:95010071; PMID:7925406
C; Function: A; Reference number: S48212; MUID:95010071; PMID:7925406
C; Function: A; Redeficed to the Brooken anglogenin.
B; R; Redeficed to the Brooken and Secondary Structure of bovine angiogenin.
B; R; Redeficed to the Brooken and Secondary Structure of Dovine anglogenin.
B; R; Redeficed to the Brooken and Secondary Structure of Dovine anglogenin.
B; R; Redeficed to the Brooken and Secondary Structure of Dovine anglogenin.
B; R; Redeficed to the Brooken and Secondary Structure of Dovine anglogenin.
B; R; Redeficed to the Brooken and Secondary Structure of Dovine anglogenin.
B; R; Redeficed to the Brooken and Secondary St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1)H nuclear magnetic resonance sped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A/Pescription: hydrolyzes tRNA; induces vascularization of normal and malignant tissues (S.Superfamily: pancreatic ribonuclease (S.Superfamily: pancreatic ribonuclease) (S.Superfamily: pancreatic ribonuclease) rucleic acid degradation. F60-68/Region: receptor binding #status predicted F74.41.115/Active site: His, Lys, His #status predicted F71-82,40-93,58-108/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N'Alternate names: RNase 1; RNase A
C'Species: Myocastor coypus (nutria, coypu)
C'Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C'Accession: A00822
R'van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim: Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla A;Reference number: A90612; MUID:77065676; PMID:99886
A;Accession: A00822
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 DEYCENIAMKNERLTRPCKDRNTFIHGNKNDIKAICE----DRNGQPYRGDLRISKSEFQI
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                                                                                                                                                                                                                                                                                      RiMaes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, FEBS Lett. 241, 41-45, 1988
A;Title: The complete amino acid sequence of bovine milk angiogenin.
A;Reference number: 802001; MUID:89065101; PMID:3197838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 125;
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R;Bond, M.D.; Strydom, D.J.
Biochemistry 28, 6110-6113, 1989
A;Title: Amino acid sequence of bovine angiogenin.
A;Reference number: A32474; MUID:89375344; PMID:2775757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch
1 Similarity 34.0%; Pred. No. 7.9e-06;
33; Conservative 14; Mismatches 32;
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                                                                                                                                                                                                                                                     A; Experimental source: plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-125 <MAE>
A;Experimental source: milk
                                                                                                                                                                                  A; Molecule type: protein A; Residues: 1-125 <BON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein A;Residues: 1-125 <MAE>
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Best Local Similarity
                                                                                                                                                    A; Accession: A32474
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C;Accession: A00818
R;Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. C. 157, 317-323, 1976
A;Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease A;Reference number: A00818; MUID:76277855; PMID:962870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pancreatic ribonuclease (EC 3.1.27.5) - casiragua (Species: Proechimys guairae (casiragua) (Species: Proechimys guairae (casiragua) (Space: 17-Mar-1987 #text_change 30-Sep-1993 (Spacession: A00821 (Speciession: A00821 (Speciession: A00821 (Speciession: A).47; Knol, G.; Martena, B. Biochim. Biophys. Acta 705, 102-110, 1982 (A).711c: The primary structures of pancreatic ribonucleases from African porcupine and A.Reference number: A90644; MUID:83000399; PMID:7115727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anote: residues 67-78 were positioned primarily by homology with other ribonucleases C; Superfamily: pancreatic ribonuclease C; Superfamily: pancreatic ribonuclease C; Seywords: glycoprotein, pydrolase; nucleic acid digestion; pancreas F;12.41,119/Active site: His, Lys, His #status predicted F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas F;12,41,119/Active site: His, Lys, His #status predicted F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------TISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N;Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TISEFYLSDCNVTSRP----CKYKLKKSINTFCVTCENQ--APVHF 98
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C'Superfamily: pancreatic ribonuclease
C'Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
E'12.41,119/Active site: His, Lys, His #status predicted
F'12.44,10-95,58-110,65-72/Disulfide bonds: #status predicted
F'34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                               28;
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                                                                                                                                                                                                         Score 126; DB 1;
Pred. No. 1.3e-05;
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28.6%; Pred. No. 1.6e-05;
ilve 15; Mismatches 42;
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us-09-961-400-11.rpr

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9
                                                                                                                                                               1 SDWLTFOKKHL-----TNTRDVDCNNIMSTNLF---HCKDKNTF1YSRPEPVKAIC-KGI 51
                                                                                                                                                                                        52 IASKNVLTT----SEFYLSDCNVTSR----PCKYKLKKSTNTFCVTCENQ--APVHF 98
                                                                                                                              20; Gaps
                                                                                 20.3%; Score 117; DB 1; Length 128; 28.0%; Pred. No. 0.0001; live 21; Mismatches 44; Indels
C;Keywords: hydrolase; nucleic acid digestion; pancreas F;12,41,119/Active site: His, Lys, His #status predicted F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                    Best Local Similarity 28.03
Matches 33; Conservative
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Angiogenin - rabbit
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Species: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999
C.Accession: S29833, B43825
B.Bond, M.D.; Strydom, D.J.; Vallee, B.L.
B.Bond, M.D.; Strydom, D.J.; Vallee, B.L.
A.Fitle: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernme A.Reference number: S29833, MUID:93192291; PMID:8448182
A.Scatus: preliminary
A.Status: preliminary

RESULT 15 B43825

A,Molecule type: protein A,Residues: 1-125 <BON> A,Note: submitted to the Protein Sequence Database, December 1992 C,Superfamily: pancreatic ribonuclease C,Keywords: pyroglutamic acid F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

8; Query Match 20.1%; Score 116; DB 1; Length 125; Best Local Similarity 31.2%; Pred. No. 0.00013; Matches 24; Conservative 13; Mismatches 32; Indels

Gaps

30 CKDKNTFIYSRPEPVKAICK---GIIASKNV-LTTSEFYLSDCNVTS----RPCKYKLKK 81 

ð Д δ

82 SINTECUTCENDAPUHE 98

99 GSRNIVIACENGLPVHF 115

Search completed: May 7, 2004, 21:54:54 Job time : 9.43686 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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ני	May 7, 2004, 21:30:40 ; Search time 5.25351 Seconds
OM protein - protein search, using sw model	, 21:30:40 ; S
search,	7, 2004
protein	May
OM protein -	Run on:

(without alignments) 1030.796 Million cell updates/sec	US-09-961-400-11 577
	US-09-5
	score:
	Title: US-C

Sequence: 1 SDWLFFQKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

SUMMAKIES	ID Description	RN30 RANPI P22069 rana pipien	P11916 rana	P18839 rana	A P14626 rana c	P80287	P00680 galea	Q64438		N P10152	P00676		Q8wn63	_CAVPO P00679	P04059	P21570	A Q8wn64	P00675	P00677	P31347	A Q8wn65	ILPAM P00672	O8hzq0 pan t	HUMAN 203950	PANTR Q8wme8 pan t	ISE 035290 mus	PIG P00671	HYSCR	P00656		G	P00674	
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æ	Query Match Length	95.5		48.6	45.8	25.0	22.9	22.6	22.6	22.2	21.8	21.7	21.1	20.8	20.8	20.7	20.5	20.5	20.3	20.1	19.9	19.8	19.7	19.6	19.6	19.6	19.4	19.4	19.4	19.4	19.3	19.2	
	Score	551	287	280.5	264.5	144	132	130.5		128	126	125	121.5	120	120		118.5	118	117	116	115	114	113.5	113	113	113	112	112	112	112	111.5	111	
	Result No.		7	٣	4	Ŋ	9	7	æ	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	•

123 1 ANGI PIG 124 1 RNPA_CAVPO 141 1 RNBR_GIRCA 146 1 ANGI SAGOE 151 1 RNBR_AXIPR 156 1 ECP2 MOUSE 123 1 ANGZ_BOVIN 124 1 RNP_ARIPA 124 1 RNP_SHEEP 124 1 RNP_SHEEP 125 1 RNF_SHEEP 126 1 RNF_SHEEP	P31346 sus scrofa P97426 mus musculu	P00678 cavia porce Q29542 giraffa cam	O8wn62 saguinus oe P87350 axis porcin	P97425 mus musculu p80929 hos tannis	P07847 aepyceros m	P00668 antilocapra P00661 ovis aries	046529 saimiri sci
23 1 2 2 3 1 2 2 3 1 2 2 3 1 2 2 3 1 2 2 3 1 2 3 2 3	ANGI PIG ECP1 MOUSE	RNPA_CAVPO RNBR_GIRCA	ANGI_SAGOE RNBR_AXIPR	ECP2_MOUSE	RNP AEPME	RNP_ANTAM RNP_SHEEP	RNS6_SAISC
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## ALIGNMENTS

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PRT;	ed) sequence update) annotation updat	Rana pipiens (Northern leopard frog). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Barrachia; Anura; Neobatrachia; Ranoidea;		985896; Shogen K.;	Anti-tumor Homology to [1991].			ng and	kana pipiens		.7 ANGSTROMS)	MEDLINE=94166079; PubMed=8120892; Mosimann S.C., Ardelt W., James M.N.G.;	ograph nti-tu	J. Mol. Biol. 236:1141-1153(1994).	against several tumor cell lines in vitro, as well as anti	in Vivo. it exhibits a ribonuci molecular weight ribosomal RNA.				; 1. PANCREATIC;	ease;	PYRROLIDONE		
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STANDARD;	19, Creat 28, Last 41, Last	chor		ubMed S.M.	mbryo 245-2	NG.	ubMed=1	lar m	rotel	(1992	HY (1	ubMed lt W.	y cry	141-1 prot	tumo	ibits t rib	TAGE: ongs	4. · RNaseA	eA; 1	se Pc NASE	End lic a	101	31	<b>68</b>
STAN	(Rel. 1 (Rel. 2 (Rel. 4	ins (Northern leopard Metazoa, Chordata; ' Batrachia; Anura; Ne	4. 	31; P ulski	acid sequence and early emb . Chem. 266:24	ODELI	56; P John	olecu	antitumor protein ";	2-400	OGRAP	79; P Arde	X-ra	236:1 Basic	veral	veigh	DEVELOPMENTAL STAGE: Early SIMILARITY: Belongs to the	10NC; 31-JAN-94.	rnas	SM00092; RNASE PC;	uclease; Endonucarboxylic acid	, 40	42	19 30
н	$\sim$	ens (	D=840	bryo; 10931 , Mik	nd ea Chem.	URE M	30661 S.C.,	ive m	antitu ";	14:39	STALL	41660 S.C.,	1.7 A	iol.	st se	vo. 1	OPMEN	.; 31-	, 4.000 2.000 CT	00092 PS001	; Nuc		мб	чю
T 1 RANPI RN30 RANPI	FZZUB3; 01-AUG-1991 01-FEB-1994 28-FEB-2003 P-30 profein	Rana pipiens Bukaryota, M Amphibia, Ba	NCBL TAXID=8404; [1] SEQUENCE.			<pre>[2] 3D-STRUCTURE MODELING</pre>	MEDLINE=93066156; PubMed=1438177; Mosimann S.C., Johns K.L., Ardelt	James M.N.G.; "Comparative molecular modeling	•	Proteins 14:392-400(1992) [3]	X-RAY CRYSTALLOGRAPHY	MEDLINE=94166079; PubMed=8120892; Mosimann S.C., Ardelt W., James M	ined	FUNCT	again	molec	DEVEL	PDB; 10NC; 31-JAN-94.	Pfam; PF00074; rnaseA; 1. Prohom: Ph000535: RNaseA.	SMART; SM PROSITE;	Hydrolase, Nuclease, Endonuclease, Pyrrolidone carboxylic acid.	MOD RES ACT SITE	ACT_SITE ACT_SITE	DISULFID
RESULT 1 RN30_RANPI ID RN30_RA	0110 0110 01110 011110	Rana Eukar Amphi	SEQU	TISS MEDI Arde	"Amino oocytes J. Bio]	[2] 3D-8	MEDI Mosi	Jame "Con	a novel	Prot	X-R	MEDI	"Ref	,	•			PDB;	Pfan	SMART; PROSITE	Hydı	ACT	ACT	DIST D <b>IS</b> T
RESULT RN30_R ID_R	2555	8888	RR	REKE	점점점	RN RP	RA RA	R.F.	RI	R. R.	RP.	Z Z	RT	报인	888	388	ខ្ល	H H	E E	8 B B	<b>₹</b>	FT	FT	H H

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01-0CT-1989 (Rel. 12, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Ribonuclease, occytes precursor (BC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
                                                                                                                                                                                                        2 DWLTFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H., Takayanagi G., Hakomori S.;
Takayanagi G., Hakomori S.;
"Amino acid sequence of sialic acid binding lectin from frog (Rana
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           ALBORDANIES SEES, PubMed=8497370;

Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;

The Rana catesbelana ror gene encoding a cytotoxic ribonuclease.

Tissue distribution, cloning, purification, cytotoxicity, and active residues for RNase activity.";
                                                                                                                                                                                                                                                                                                                                                                    Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
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                                                                                                                                                                        Length 104;
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                                                                                                                                                                                                                                         62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                                       11845 MW; 22A753C2F9E566B4 CRC64;
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                                                                                                                                                                       Score 551; DB 1;
Pred. No. 3.5e-52;
                                                                                                                                                                                                                                                                                                    133 AA
                                                                                                                                                                                       2; Mismatches
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MEDLINE=92220613; PubMed=1373237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 20:1371-1377 (1992).
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                residues for RNase activity.",
J. Biol. Chem. 273:6395-6401(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=E9g;
MEDLINE=87299649; PubMed=3304421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catesbeiana) eggs.";
Biochemistry 26:2189-2194(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oocytes."
                                                                                                                                                                       95.5%;
96.1%;
                                                                                                                                                                             Best Local Similarity 96.1
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                    STANDARD;
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58
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                                                                                                                                                        104 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
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ش
                                                                                                                                                                                                                     MEDLINE=9847383; PubMed=9761686;
Chang C.-F., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
The solution structure of a cytotoxic ribonuclease from the occytes of Rana catesbelana (bullfrog).";
J. Mol. Biol. 283:231-244(1998).";
J. Mol. Biol. 283:231-244(1998).";
-!-FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine residues with a 3'flanking quanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin. It is cytotoxic against several tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00092; RNASE PC; I.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure; Signal; Pyrrolidone carboxylic acid.
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TISSUE=Egg;
MEDLINE=93192604; PubMed=8448385;
MITLA K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
Takayanagi Y., Hakomori S., Titani K.;
"Ribonuclease activity of sialic acid-binding lectin from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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49.1%; Pred. No. 7.4e-24;
live 16; Mismatches 32; Indels
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PYRROLIDONE CARBOXYLIC ACID.
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PDB; 1BC4; 28-OCT-98.
PDB; 1MO7; 21-JAN-03.
Interpro; IPR01427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                          catesbelana eggs.";
Glycobiology 3:37-45(1993).
                                                                                                                                                                         (5)
STRUCTURE BY NMR OF 23-133
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            61
DWLIFQKKHLINIRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DWLTFQKKHLINTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
                                                                                                                                                                                                                                                                                            J. Biochem. 108:139-143(1990).
-!- FUNCTION: The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin preferentially agglutinate a large variety of tumor cells, but it does not agglutinate non-transformed cells and erythrocytes.
-!- SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                 TISSUE=Egg;
MEDLINE=91035319; PubMed=2229005;
Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
Takayanagi Y., Titani K.;
                                                                                                                                                                                                                                                                        "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sialic acid-binding lectin (BC 3.1.27.-).
Rana japonica (Japanese reddish frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LITSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 LITSEFYLSDC---NVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 280.5; DB 1; Lews...
Pred. No. 3e-23;
Triffhes 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE Por 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; Pytrolaone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111
12326 MW; FDEBDDF3834ED679 CRC64;
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SIMILARITY.
SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001427; RNaseA. Pfam; PF00074; rnaseA; 1.
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                                                                                                             STANDARD;
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104
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HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                     NCBI_TaxID=8402;
                                                                                                            LECS RANJA
P18839;
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ACT_SITE
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111 AA

PRT;

STANDARD:

RNPL RANCA

RNPL RANCA ID RNPL RA AC P14626

RESULT

P146<u>2</u>6;

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2 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
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Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
Okazaki T., Ohgi K., Irie M.;
"Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Endomucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphate intermediates.
with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
IF; JX0085; JX0085.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                               Eukaryota, Metazoa, Chordaťa, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
NCBI_TaxID=8517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao W., Beintema J.J., Hofsteenge J.; "The amino acid sequence of iguana (Iguana iguana) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (BC 3.1.27.5) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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; Pred. No. 1.5e-21;
19; Mismatches 37;
01-APR-1990 (Rel. 14, Created)
01-FFB-1994 (Rel. 28, Last sequence update)
08-FBB-2003 (Rel. 41, Last annotation update)
Ribonuclease, liver (EC 3.1.27.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
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                                                                                                                                                          Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROBABLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eur. J. Biochem. 219:641-646(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94139745; PubMed=8307028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iguana iguana (Common iguana).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biochem. 106:729-735(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111
12461 MW;
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                                                                                                                                                                                                                                                                             NCBI_TaxID=8400;
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ANGR MOUSE
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DISULFID
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ACT_SITE
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VARIANT
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          DISULFID
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To office amino acid sequences with those of two close relatives:

To applear and cuis ribonuclease, and the cappear and cuis ribonuclease of two close relatives:

To MOI. Evol. 19:145-152(1983).

To MOI. Evol. 19:145-152(1983).

To MOI. Evol. 19:145-152(1983).

To Superlation and 3'-phosphodigonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.

To Superlation Secreted.

To Superlati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DWLTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAIC--KG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Gaps
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
-!- SUBCELIULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR; $41111; $41111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Galea.
NCBI TaxID=10146;
                                                                                                                                                                                                                                                                                                                                     PROSITE: PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
MOD RES 1 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 IIASKNVLTISE-FYLSDC----NVTSRPCKYKLKKSTNTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6072FB5B7B15BD5A CRC64;
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                                                                                                                                                                                 HSSP, P00656; 1LSQ.
InterPro; 1PR001427; RNaseA.
Pfam, PF00074; RNBOAGA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNASEA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                  SMART; SM00092; RNASe Pc;
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106
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Best Local
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RNP_GALMU
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          KARARA BERNAL BE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SDWLTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAICKG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                       SSAMKFOROHMDSDGHPDTNTN--YCNEMMVRRSMTQGRCKPVNTFVHEPLEAVQAVC-- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 IIASKNV------LTTSEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCEN--QA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=129; TISSUB=Liver;
STRAIN=129; TUBMed=8530072;
Brown W.E., Nobile V., Subramanian V., Shapiro R.;
"The mouse angiogenin gene family: structures of an angiogenin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                          MISSING (IN 1/3 OF THE MOLECULES). 609C7E251A7BBA25 CRC64;
                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANGIOGENIN. RELATED PROTEIN.
PYRROLDONE CARBOXYLIC ACID (BY SIMILARITY).
                                                                                                                                                                                                                                                                            Length 124;
                                                                                                                                                                                                                                                                         22.9%; Score 132; DB 1; 30.6%; Pred. No. 2.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                              18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERMY PRO074; rnaseA, 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNase Pc; 1.
SMART; SM00092; RNASE PC; 1.
Signal; Hydrolase; Nuclease; Bronuclease;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiogenin-related protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein gene and two pseudogenes.";
Genomics 29:200-206(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                         MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U22519; AAA91367.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P03950; 1A4Y.
MGD; MGI:104984; Angrp.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                      13870
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
     84
95
110
72
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411
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                                                                                                                                                                                                                         124 AA;
                                                                                                                                                                                                                                                                                                  Local Similarity
nes 38; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 PVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVHF 98
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37
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138
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81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                      ANG1 OR ANG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chang S.-I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Milk;
                                                                                                                                                                                                                                                                                            ANGI BOVIN
ACT_SITE
ACT_SITE
ACT_SITE
DISÜLFID
                                                                                                                                                                                                                              98
                                                              DISULFID
                                                                                                   Query Match
                                                                           SEQUENCE
                                                                                                                Local
                                                                                                                                                                                                                                                                   RESULT 9
ANGI BOVIN
                                                                                                                Best
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                                                                                                                             3,
                                                                                                                                                                   63 CKDVNTFIHDTKNNIKALCGKKGSPYGRNLRISKSRFQVTTCTHKGRSPRPPCRYRASKG 122
                                                                                                                                                     ---PCKYKLKKS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nate evolution..;
Biol. Evol. 19:438-445(2002).
Biol. Evol. 19:438-445(2002).
Biol. Evol. 19:438-445(2002).
FUNCTION: May function as a tRNA-specific ribonuclease that binds for actin on the surface of endothelial cells; once bound, angiogenin is endocycosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity).
SUBCELIULAR LOCATION: Secreted.
SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: AF441664; AAL61646.1; -.

EMBL: AF441664; AAL61646.1; -.

PEAM: PF0001427; RNaseA.

PRINTS; PR00794; RIBONUCLEASE.

PRODOM: PD000535; RNaseA; 1.

PROSITE; PS00127; RNASE PC: 1.

PROSITE; PS00127; RNASE PC: 1.

PROSITE; PS00127; RNASE PANCREATIC; 1.

PROSITE; PS00127; RNASE PANCREATIC; 1.

PROFITE; PS00127; RNASE PANCREATIC; 1.

PROFITE: PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang J., Rosenberg H.F.; "Diversifying selection of the tumor-growth promoter angiogenin in
                                                                                                                                                                                                                                                                                                                                                                                Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anglogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
ANG OR RNASES.
                                                                                                   22.6%; Score 130.5; DB 1; Length 145; 38.2%; Pred. No. 4.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
                                                                                                                            29; Indels
                                                                                                                                                      CKDKNTFIYSRPEPVKAIC--KGIIASKNV-LTTSEFYLSDCNVTSR
 BY SIMILARITY.
29AGEBB14429C4AD CRC64;
                                                                                                                              11; Mismatches
                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21918422; PubMed=11919285;
   Cercopithecinae; Cercopithecus.
                                                                            16612 MW;
                                                                                                                                                                                                                               123 FRYIIIGČENGWPVHF 138
                                                                                                                                                                                                       INTECVICENQAPVHF 98
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                              STANDARD;
   37
64
137
104
130
  37
644
137
50
63
145 AA;
                                                                                                                 Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9534;
                                                                                                                              29;
                                                                                                                                                                                                                                                                                              CERAE
                                     DISULFID
  ACT_SITE
ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primate (
Mol. Bio]
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MOD_RES
                                                                DISULFID
                                                                            SEQUENCE
                                                                                                     Query Match
                                                                                                                  Local
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                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                         STILLIS
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5 TFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIC---KGIIASKNV-LTT 60
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                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89118214; PubMed=3064806;
Bond M.D., Vallee B.L.;
"Isolation of bovine angiogenin using a placental ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95224057; PubMed=7708754; Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.; Crystal structure of bovine angiogenin at 1.5-A resolution."; proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89065101; PubMed=3197838;
Maes P., Damart D., Rommens C., Montreuil J., Spik G., Tartar !
"The complete amino acid sequence of bovine milk angiogenin.";
FEBS Lett. 241:41-45(1988).
                                                                                                                                                                                                  22.6%; Score 130.5; DB 1; Length 146; 30.7%; Pred. No. 4.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloming, sequencing, and expression of bovine angiogenin."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR. MEDLINE=96280645; PubMed=8688423; Lequin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
                                                                                                                                                                                                                                                  30; Indels
                                                                                                                                                   27860112E85B8DF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          97
                                                                                                                                                                                                                                                                                                                                                                                                        61 SEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P10152; Q9GKP9;
01-MAR-1989 (Rel. 10, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
PAR-2004 (Rel. 43, Last annotation update)
Angiogenin-1 precursor (EC 3.1.27.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bond M.D., Strydom D.J.;
"Amino acid sequence of bovine angiogenin.";
Biochemistry 28:6110-6113(1989).
                                                                                                                                                                                                                                                       17; Mismatches
SIMILARITY. SIMILARITY. SIMILARITY.
                                                                       SIMILARITY.
SIMILARITY.
SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89375344; PubMed=2775757;
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  BY BY BY BY BY BY BY BY
37 BY
64 BX
138 BY
105 BY
116 BY
131 BY
1644 MW;
                                                                                                                                                                                                                                                          31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibitor binding assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                           53 TMRRRHLTSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 24-148.
TISSUE=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 24-148.
                                                                                                                                                                                                                                  Similarity
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MEDLINE=76277855; PubMed=962870;
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14267 MW;
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21-JUL-1986 (Rel. 01, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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110
72
12
411
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DISULFID 26 8
                                                                                                                                                                                                                                                                                                                                                                 PIR; A00822; NRCU
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40
58
12
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DISULFID
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ALD RNNP B
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               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ŋ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVDCNNIMSTNLF--HCKDKNTFIYSRPEPVKAICKGIIASKN-----VLTTSEFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
RNASE1 OR RNS1.
Myocastor coypus (Coypu) (Nutria).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Myocastoridae;
"Solution structure of bovine angiogenin by 1H nuclear magnetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16969 MW; B7999124CBB523DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSO0127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 SDC---NVTSR-PCKYKLKKSTNTFCVTCENDAPVHF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.2%; Score 128; DB 1; 34.0%; Pred. No. 8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDB; IGIO; 07-DEC-96.
InterPro; IPR001427; RNaseA.
Ffam; PP00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00992; RNASE PC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF135124; AAG47631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 34.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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50
63
148 AA;
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P00676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
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BD 21-JU
DT 21-JU
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DT 21-JU
DT 28-PB
DE Ribon
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GN RNASE
GC BUKAR
CC BU
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6 FOKKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF 98
MEDIINE-77065676; PubMed=999896;
van den Berg A., van den Hende-Timmer L., Beintema J.J.;
van den Berg A., van den Hende-Timmer E., Beintema J.J.;
pancreatic ribonuclease.";
Biochim. Biophys. Acta 453:400-409(1976).
-!- CATALYTIC ACITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2', 3'-cyclic phosphate intermediates.
-!- SUBCELULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Emmens M., Welling G.W., Beintema J.J.,
"The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
ribonuclease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleoside 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Mysticeti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
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-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside in prosphates and 3'-phosphooligonucleotides ending in C-P or with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family. PIR; A00818; NRWHK.
HSSP; P00656; 1SRN.
                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LINKED (GLCNAC, . .).
4EB924E52B445832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 21.8%; Score 126; DB 1; Similarity 29.9%; Pred. No. 1.1e-06; 35; Conservative 18; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                     HSSP; P00656; ISRN.
InterPro; IRRO01427; RNaseA.
Pfan; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; P0000535; RNaseA; 1.
SWART; SM0092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endonuclease;
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Gaps

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
ANG OR RNASES.
                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21918422; PubMed=11919285;
                                                                                                                                                                                                                                                                                                                                   Macaca mulatta (Rhesus macaque)
      Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF441667; AAL61649.1; -
                                                                                                                                          21.7%;
InterPro; IPR001427; RNaseA.
                                                                                                                                                    28.68;
                                                                                                                                                                             4 LTFQKKHLTNTRDVD--
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                             Cercopithecinae; Macaca.
                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9544;
                                                                                                                                                            34;
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                                                                                                                                           Query Match
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5 TFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIC---KGIIASKNV~LTT
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van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastra W.,
Beintema J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              structure and glycosidation.";
Eur. J. Biochem. 75:91-100(1977)
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
blosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cavia porcellus (Guinae pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
                                                               Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
SIGNAL
                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SIMILARITY: Belongs to the pancreatic ribonuclease family. PIR; A00825; NRGPB. HSSP; P00656; 1SRN. InterPro; IPRO01427; RNASEA.
                                                                                                                                                                                                                                                                                      DB 1; Length 146;
                                                                                                                    (BY
                                                                                                                                                                                                                                                                                                                       32; Indels
                                                                                                                  PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                    E39A89215DB2A2A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 SPFQVITCKLRGGSPRPPCQYRAIRGSRNIVVGCENGLPVH 138
                                                                                                                                                                                                                                                                                                                                                                                                                         61 SEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVH 97
ProDom, PD000535; RNaseA; 1.
SMART; SM0092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PS PANCERATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Glycoprotein.
                                                                                                                                                                                                                                                                                    21.1%; Score 121.5; DB 1
28.7%; Pred. No. 3.9e-06;
iive 17; Mismatches 32
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PRINTS; PR00794; RIBONUCLEASE.
                                                                                                                                                                                                                                                      16301 MW;
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29; Conservative
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138
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146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNPB CAVPO P00679;
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SEQUENCE
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MOD_RES
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Matches 2
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                                                                                                                                                                                                                                                                                                                                                          --- CNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK 55
                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 NVLCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                           56 NVL-----TISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang J., Rosenberg H.F.;

Zhang J., Rosenberg H.F.;

"Diversifying selection of the tumor-growth promoter angiogenin in primate evolution."; 19438-445 (2002).

-!- EVOLTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity).

-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                                      Score 125; DB 1; Length 124;
Pred. No. 1.4e-06;
                                                                                                                                                                                                                                      (30%)
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                                                                                                                                                                                                                                                                                                                         42;
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15; Mismatches
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| SSAMKEQRQHMDPEGSPSNSSNY-CNVMMIRRNMTQGRCKPVNTFVHESLADVQAVC---
                                                                                                                                                                                                                                                                                             IASKNVL-----TISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--AP
                                                                                                                                                                30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proechimys guairae (Casiragua).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Echimyidae; Proechimys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
                                                                                                                                                                Indels
                                                                    A2F4101A1A33E93B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2DB58093A9D3C936 CRC64;
                                                                                                                                                                37;
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                                                                                                            20.8%; Score 120; DB 1;
28.5%; Pred. No. 4.9e-06;
ive 21; Mismatches 37;
    N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , DB 1;
4.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=83000399; PubMed=7115727;
21 N-
34 N-
64 L
14406 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
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HSSP; P00656; 1SRN.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00092; RNASe Pc; 1
PROSITE; PS00127; RNASE PAN
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
21
34
64
128 AA;
                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10163;
                                                                                                                                                                                                                                                                                                                                                                                                                              118 VHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Pancreas;
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CARBOHYD
CARBOHYD
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                                                                 SEQUENCE
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RNP_PROGU
                                                                                                                                                         Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTION PROPERTY OF THE PROPERY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
                           64 PCKNGQSNCYESTSNWHITDCRLTSNSKFPDCLYRTSQEEKSIIVACEGNPYVPHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LITSEFYLSDCNVTSR----PCKYKLKKSINTFCVTCENQ--APVHF 98
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93192291; PubMed=8448182;
Bond M.D., Stryddm D.J., Vallee B.L.;
"Characterization and sequencing of rabbit, pig and mouse
angiogenins: discernment of functionally important residues and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydrolyzing cellular tRNAs.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                         Last annotation update)
(EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91025023; PubMed=2222458;
Bond M.D., Vallee B.L.;
"Isolation and sequencing of mouse angiogenin DNA.";
Biochem. Biophys. Res. Commun. 171:988-995(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                     145 AA
                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                           01-MAY-1991 (Rel. 18,
01-MAY-1991 (Rel. 18,
15-MAR-2004 (Rel. 43,
                                                                                                                                                                                                                                                                                                               Angiogenin precursor
                                                                                                                                                                                                                                                                                                                                                               (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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P21570;
58
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7;

Gaps

28;

36; Indels

Pred. No. 4.9e 18; Mismatches

35; Conservative

Best Local Similarity

Matches

à

57

6 FQKKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV

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5;
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 KHLTNTRDVD-----CNNIMSTNLF--HCKDKNTFIYSRPEPVKAIC--KGIIASKN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 20.7%; Score 119.5; DB 1; Length 145; Best Local Similarity 30.8%; Pred. No. 6.3e-06; Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps
                                                                                                                                                EMBL; U22116; AAA91366.1; -.

R PIR; AA5923; AA455355.1; -.

R PRS; P03950; 1A3593.

R HSSP; P03950; 1A3593.

R InterPro; DR001427; RNaseA.

R PRINTS; PR00794; RIBONUCLEASE.

R PRODOM; P0000535; RNASeA; 1.

R PRODOM; P0000535; RNASeA; 1.

R PRODOM; P000053; RNASEA; P000053; RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANGIOGENIN.
PYRROLIDORE CARBOXYLIC ACID (BY SIMILARITY).
BY SIMILARITY.
MY 06944260BB764938 CRC64;
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145 AA;
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ACT_SITE
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Search completed: May 7, 2004, 21:53:05 Job time: 6.25351 secs

57 V-LITSEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVHF 98

δλ q

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GenCore version 5.1.6
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               Copyright
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using sw model - protein search, OM protein Run on:

May 7, 2004, 21:25:55 ; Search time 44.7895 Seconds (without alignments) 662.376 Million cell updates/sec

582 1 MSDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 US-09-961-400-13 score: Sequence: Title: Perfect

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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A Geneseq 29Jan04:\* Database

geneseqp2003as:\*geneseqp2003bs:\* geneseqp2002s:\* geneseqp2004s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CITAMADITE

i	SCORE 582 577 577 573 573 573	(17) 1	Length 105 105 104 104 127	B   D   D   D   D   D   D   D   D   D	ID AAY28871 AAY28867 AAY28869 AAY28869 AAY28865 AAY28879 AAY28879	e e e e e e e e e e e e e e e e e e e	Recombina Recombina Recombina Recombina Rana pipi
8 6 1 1 5	560 560 560 560	0 10 10 10 10	112 251 254 355	0 0 0 0 0	AAW35118 AAW35134 AAW35135 AAW35133 AAW35109	Aaw35118 R. Aaw35134 R. Aaw35135 R. Aaw35133 R.	pipien pipien pipien pipien
113 113 115	5 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2220		10000	AAW35122 AAW06544 AAW35123 AAW35125	<del>.</del>	pipien itumou pipien pipien
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2222 2223 242 254	551 551 551 551	44444		00000	AAR47303 AAW00736 AAW14065 AAW30301 AAW30301		ONCONASE Protein d Onconase Antitumou Recombina

		Aab31666 Amino aci	Abg32650 Northern	굠.	Aaw35117 R. pipien	Aaw35127 R. pipien	Aaw35131 R. pipien		Aaw35115 R. pipien	Aaw30302 Recombina	Aaw18224 Antitumou	Aab31667 Amino aci	Abg31617 Northern	~	Aaw35128 R. pipien	Aaw35121 R. pipien	Aaw35119 R. pipien	Aaw88234 Rana pipi	Aay33321 Frog lect
AAW88233	AAY33322	AAB31666	ABG32650	AAW35122	AAW35117	AAW35127	AAW35131	AAW35126	AAW35115	AAW30302	AAW18224	AAB31667	ABG31617	AAW35120	AAW35128	AAW35121	AAW35119	AAW88234	AAY33321
(1)	N	4	'n	ď	7	N	N	N	N	~	N	4	Ŋ	7	~	~	N	7	7
104	104	104	104	106	107	358	365	379	105	104	104	104	104	107	360	111	83	83	111
94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.3		93.8	93.3	93.3	91.4	85.7	83.2	76.5	76.5	49.3
551	551	551	551	551	551	551	551	551	549	548	546	543	543	532	499	484.5	445	445	287
26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

AAY28871 standard; protein; 105 AA. RESULT 1 AAY2887 

AAY28871;

(first entry) 25-JAN-2000

Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.

Recombinant Met(-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonucleas; cytotoxic fusion protein; cancer; frog; autoimmune disease; RNase.

Rana pipiens. Synthetic.

Location/Qualifiers Misc-difference

/note= "Met not found in wild type RaPLR1" /note= "Wild type Gln replaced with Ser" Misc-difference

W09950398-A2

07-0CT-1999.

99WO-US006641. 26-MAR-1999; 98US-0079751P. 27-MAR-1998; (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Newton DL; Rybak SM,

WPI; 1999-610847/52. N-PSDB; AAZ08129

for New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.

Claim 34; Page 61; 71pp; English.

The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which

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can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadorrophin (hCG) effective against Kaposi,'s sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an Neterminal methionine due to the presence of a signal peptide that is terminal wethionine due to the presence of a signal peptide that is proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Met at position 1. Carboxy terminal end of recombinant KaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hGG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal
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                                                                                                                                                                                                                                                                   1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                                                                                                                                                                                                                                                                                          Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase; covalantly bound; LiZ antibody; ligand binding moisty; cancerous B ce: Kaposi,'s sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                    0;
                                                                                                                                                                                               Length 105;
                                                                                                                                                                                                                                                                                                                                    61 ISEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant ribonucleases, used for killing target cel
treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                             Score 582; DB 2;
Pred. No. 2.6e-62;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY28867 standard; protein; 105 AA.
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                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-610847/52.
                                                                                                                            autoimmune diseases
                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                           Sequence 105 AA;
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rana pipiens.
Synthetic.
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                                                                                                                                                                                                                            Matches 105;
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                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant Rana pipiens ribonuclease, RaPLRI Gln1Ser; covalently bound; Liz antibody, 11gand binding molecty, CD22, cancerous B cell; frog; Kaposi, s sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase;
methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cyrotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                         MQDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
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                                                                                                                                                                          Gaps
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                                                                                                                                         DB 2; Length 105;
                                                                                                                                                                                                                                                                          TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                              TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant RaPLR1 Gln1Ser amino acid sequence.
                                                                                                                                     Score 578; DB 2,
Pred. No. 8e-62;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                                                                                                                                                                                                                                                           AAY28870 standard; protein; 104
                                                                                                                                       99.3%;
99.0%;
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                                                                                                                                                                       104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune disease.
                                                                                                                                     Query Match
Best Local Similarity
                                                                                                     Sequence 105 AA;
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Misc-difference
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                                                                                                                                                                       Matches
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expression of ribonuclease allows the proteins to be fused ligand binding moieties to form cytotoxic fusion proteins. Used for treatment of cancer and autoimmune diseases

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Gaps

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1; Indels

Score 575; DB 2; Pred. No. 1.8e-61; 1; Mismatches 1;

98.8%;

103; Conservative

Local Similarity

Query Match Matches

Sequence 105

5555×8

Length 105;

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                                                                                                                           SDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "(His)6 histidine tag attached to N-terminal Met"
                                                                                                                                                                                                                                                                                                                       Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1; CDD22; covalently bound; LL2 antibody; ligand binding moiety; RNase; cancerous B cell; Kaposi's sarcoma, human chorionic gonadetrophin, hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
                                                                                                       SDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                   Gaps
proteins. They can be used for treatment of cancer and autoimmune diseases
                                                                                   ..
0
                                                          Length 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Met not found in wild type RaPLR1"
                                                                                                                                                    SEFYLSDCNVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                  SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                   Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
                                                            Score 577; DB 2;
Pred. No. 1e-61;
                                                    99.1%; Sco...
100.0%; Pred. No. 10....
--- 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        cancer; frog; autoimmune disease
                                                                                                                                                                                                                                  AAY28869 standard; protein; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US006641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0079751P
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                                                                                 Conservative
                                                          Query Match
Best Local Similarity
Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                     Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                             Rana pipiens
Synthetic.
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The present sequence is Rana pipiens liver ribonuclease (RapLR1) protein. Carboxy terminal end of RapLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD2 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic jusion proteins. They can be used for treatment of cancer
                 Rana pipiens liver ribonuclease, RaPLR1, covalently bound, LL2 antibody, ligand binding moiety, CD22; cancerous B cell; Kaposi's Sarcoma; frog; human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 104;
                                                                TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                     98.5%; Score 573; DB 2; L
ilarity 100.0%; Pred. No. 3.2e-61;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                  Rana pipiens liver ribonuclease (RaPLR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                      AAY28865 standard; protein; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 55; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US006641.
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ08124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9950398-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                           Rana pipiens
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                                                                                                                                                                                                                   AAY28865;
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Local Similarity

Best Local Sim: Matches 103;

The present sequence is a recombinant Rana pipiens ribonuclease protein (Raphal) with Met at position 1 attached to (His)6 tag and Met24Leu. Carboxy terminal end of recombinant Raplal has a covalently bound ligand binding molety, which can be a Li2 antibody directed against CD22 on cancercus B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble

New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.

Rybak SM, Newton DL; WPI; 1999-610847/52. N-PSDB; AAZ08127. Claim 4; Page 59; 71pp; English.

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Rana
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                                                                                                                                                                                                                                                                                                                                                                                             Rana pipiens ribonuclease Clone 5alb; RaPLR1; covalently bound; RNase; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase; Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer; recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
          62
                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
DWLIFQKKHLINIRDVDCNNIMSINLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLITS
                              EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .23
/label= Signal peptide
/note= "Putative"
                                                                                                                                                                                                                                                                                                                                                        Rana pipiens Clone 5alb ribonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                               AAY28879 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 69; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US006641
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                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                     AAX28879
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AAX28879
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AAX28879
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98.5%; Score 573; DB 2; Length 127; larity 100.0%; Pred. No. 4.1e-61; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 103; Conserv

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant Rana pipiens ribonuclease; RaPLR1 Met23Leu; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a recombinant Rana pipiens ribonuclease (RaPiRI) protein with Met23Leu. Carboxy terminal end of recombinant RaPIRI has a covalently bound ligand binding moiety, which can be a LLZ antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytochoxic fusion proteins. They can be used for treatment of cancer and autoimmune
  62
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                            for
DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGJIASKNVLTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g.
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                                                                                                                        /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 7.3e-61;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant RaPLR1 Met23Leu amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                   AAY28866 standard; protein; 104 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease.
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pipiens
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Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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diseases
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novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to none and also lower immunogenicity in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribonuclease molecules based on native Onconase - used for killing cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAW35125 to AAW35135 represent recombinant fusion proteins (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 MSDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                                                                                                                                                           RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion; tumour cell growth; frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion; tumour cell growth; frog.
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                                                                                                              3. pipiens recombinant RNase rOnc fusion protein 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.2%; Score 560; DB 2; I 96.2%; Pred. No. 3.7e-59; iive 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wlodawer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                       97WO-US002588
                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0011800P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               particularly tumour cells.
                                                                    (first entry)
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tes 101; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 251 AA;
                                                                                                                                                                                                                            Rana pipiens.
                                                                                                                                                                                                                                                                                                 WO9731116-A2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ribonucleases have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribonuclease molecules based on native Onconase - used for killing cells,
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DWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases havincreased cytotoxic activity compared to nonc and also lower immunogenicity in humans.
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                                                                                                                                                                                                                                                                                                                                                                                   RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion; tumour cell growth; frog.
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                                                                        BFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                            63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC

    R. pipiens recombinant RNase protein NLSMetSerrOnc.

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                                                                                                                                                                                                   AAW35118 standard; protein; 112 AA
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Best Local Similarity
Matches 101; Conserv
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Gaps

Indels

Length 251;

206

AAW35134 ID AAW3

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N-PSDB; AAT94967
            21-FEB-1996;
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Synthetic.
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                                                   Rybak SM,
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Matches
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                                                                                                                                                                                                                                      Sequences AAW35125 to AAW35135 represent recombinant fusion proteins (ronc) which are modifications of the RNase Onconase (RTW) (nonc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient underspoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new
                                                                                                                                                                                                                                                                                                                                            ribonucleases have increased cytotoxic activity compared to nonc and also lower immunogenicity in humans
                                                                                                                                                                                           Ribonuclease molecules based on native Onconase - used for killing cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSDWLIFQKKHLINIRDVDCNNIMSINLFHCKDKNIFIYSRPEPVKAICKGIIASKNVLI 60
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                                                                                                                                                                                                                                                                                                                                                                                             Length 254;
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                                                                                                                                                                                                                                                                                                                                                                                 96.2%; Score 560; DB 2; Le
96.2%; Pred. No. 3.7e-59;
Mismatches 2;
                                                                                                                                         Wlodawer A;
                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                          Boque L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW35133 standard; protein; 355
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                                                                                                                                                                                                     particularly tumour cells.
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nes 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumour cell growth; frog
                                                                                                                                         Newton DL,
                                                                                                                                                             WPI; 1997-435168/40.
                                                                                                                                                                       N-PSDB; AAT94973
                                                                                                                                                                                                                                                                                                                                                                          Sequence 254 AA;
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          pipiens
                                       WO9731116-A2
                                                                              19-FEB-1997;
                                                                                                  21-FEB-1996;
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                   Synthetic.
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          Rana
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Sequences AAW35125 to AAW35135 represent recombinant fusion proteins (rCnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclasses molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nonc and also lower immunogenicity in humans
                                                                                                                                                                                                                                                                                              Ribonuclease molecules based on native Onconase - used for killing cells,
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                                                                                                                               Wlodawer A;
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                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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96.2%; Pre
                                                                                                                                   Boque L,
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96US-0011800P
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                                                                                                                                                                                                                                                                                                                             particularly tumour cells.
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                                                                                                                                                                                             WPI; 1997-435168/40.
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nes 101; Conserv
                                                                                                                                                                                                                                N-PSDB; AAT94971
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or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nonc and also lower immunogenicity in humans

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Gaps

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2; Indels

6e-59;

Score 560; Pred. No. 6

96.2%;

Query Match 96.2 Best Local Similarity 96.2 Matches 101; Conservative

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Sequence 366 AA;

2; Mismatches

DB

Length 366;

262 MSDWITFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 321

61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 366

322

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Gaps

· 0

2; Indels

Length 355;

9

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AAW06544 standard; protein; 104

AAW06544

Antitumour protein from Rana pipiens oocytes.

(first entry)

22-AUG-1997

AAW06544;

Tumour; chemotherapy; radiotherapy; frog.

Rana pipiens WO9639428-A1

12-DEC-1996.

96WO-US008304. 95US-00467955.

(ALFA-) ALFACELL CORP

06-JUN-1995;

WPI; 1997-043063/04.

Ardelt WJ;

1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60

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(ronc) which are modifications of the RNase Onconase (RTM) (nonc). Such novel ribonuclesse molecules are highly cytotoxic and can be used alone or to form chemical conjustes or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nonc and also
                                                                                                                                                                                                                                                                                                                                                                         251 MSDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 310
            Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells.
                                                                                                                                                                                                                                                                                                                                               1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                                                                                Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
                                                                                                                                                                                                                                                                                                                                                                                                                     TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                     Score 560; DB 2;
Pred. No. 5.8e-59;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wlodawer A;
                                                     71; 90pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW35132 standard; protein; 366
                                                                                                                                                                                                                                    Lower immunogenicity in humans
                                                                                                                                                                                                                                                                                       96.2%;
96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US002588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour cell growth; frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM, Newton DL,
                                                                                                                                                                                                                                                                                                 Local Similarity
nes 101; Conserv
                                                     Disclosure; Page
                                                                                                                                                                                                                                                              Sequence 355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-1996;
                           particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9731116-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW35132;
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rybak
                                                                                                                                                                                                                                                                                                                  Matches
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RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
R. pipiens recombinant RNase rOnc fusion protein 8.
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                                                                                                                                                                                                                                                                                                                                                             protein from the generic protein in AAW18224, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW06543) that have been isolated from Rana pipiens occytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy and surgery in the
                                                                                                                                                                                                                                                                                                                                                    The present sequence is a specifically claimed example of an antitumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.5%; Score 556; DB 2; Length 104; 97.1%; Pred. No. 3.6e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                              Claim 8; Page 28; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Ribonuclease molecules based on native Onconase - used for killing cells,

(rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone

Sequences AAW35125 to AAW35135 represent recombinant fusion proteins

Disclosure; Page 74; 90pp; English.

particularly tumour cells.

WPI; 1997-435168/40.

N-PSDB; AAT94970

Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy.

Job time : 45.7895 secs

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AAW35115 to AAW35123 encode recombinant proteins (ronc) which are modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used for particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have immunogenicity in humans
      62
                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribonuclease molecules based on native Onconase - used for killing cells,
DWLIFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
                   2 DWLTFQKKHVINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
                                                                                                                                                                                                                                                                                                     RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion; tumour cell growth; frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 105;
                                                               63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                               62 BFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104
                                                                                                                                                                                                                                                                      R. pipiens recombinant RNase protein [Met-(-1)]rOnc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wlodawer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                          AAW35123 standard; protein; 105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boque L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US002588.
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                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            particularly tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rybak SM, Newton DL,
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                                                                                                                                                                                                                                                                                                                                                     Rana pipiens.
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